

Two novel closteroviruses, fig virus A and fig virus B, identified by the analysis of the high-throughput RNA-sequencing data of fig (*Ficus carica*) latex

Dongbin Park, Chul Jun Goh, Yoonsoo Hahn*

Department of Life Science, Chung-Ang University, 84 Heukseok-ro, Dongjak-gu, Seoul 06974, Republic of Korea

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Summary. – Closteroviruses (the genus *Closterovirus*, the family *Closteroviridae*) are RNA viruses that infect and cause viral diseases in many economically important plants. Genome sequences of two novel closteroviruses named fig virus A (FiVA) and fig virus B (FiVB) were identified in high-throughput sequencing data obtained from a fig latex sample. FiVA and FiVB genomes, whose lengths are 19,333 bp and 18,741 bp, respectively, were predicted to have 14 shared open reading frames, nine of which had homologs in other closteroviruses. Phylogenetic analysis confirmed that FiVA and FiVB are novel closteroviruses forming a strong subclade with fig mild mottle-associated virus within the genus *Closterovirus*. FiVA and FiVB genome sequences identified in this study are useful resources for investigating the evolution of closterovirus genome organization.

Keywords: fig virus A; fig virus B; Closterovirus; common fig; *Ficus carica*

Introduction

Closteroviruses (the genus *Closterovirus*) are plant-infecting RNA viruses of the family *Closteroviridae*, which contain three other genera (*Ampelovirus*, *Crinivirus*, and *Velarivirus*) and some unassigned species (Agranovsky, 2016; Fuchs *et al.*, 2020). Members of the genus *Closterovirus*, whose type species is beet yellows virus (BYV), infect and cause viral diseases in many economically important plants (Karasev *et al.*, 1995; Koloniuk *et al.*, 2018; Orilio *et al.*, 2018; Zheng *et al.*, 2018).

Closteroviruses have long and flexuous virions with a large positive-sense single-stranded RNA genome of

14–19 kb. The genome encodes about 10 conserved open reading frames (ORFs), including polyprotein (ORF1a), RNA-dependent RNA polymerase (RdRp; ORF1b), 6-kDa protein (p6), heat shock protein 70 homolog (Hsp70h), heat shock protein 90 homolog (Hsp90h), minor coat protein (CPm), and major coat protein (CP) (Zheng *et al.*, 2018; Fuchs *et al.*, 2020). The polyprotein is proteolytically processed into papain-like protease, methyltransferase, and helicase. The RdRp is produced as a fusion ORF1ab by the +1 ribosomal frameshift at the end of ORF1. In addition, unique ORFs that are shared by some members are also observed (Karasev *et al.*, 1995; Tzanetakis *et al.*, 2007; He *et al.*, 2015; Agranovsky, 2016; Zheng *et al.*, 2018).

High-throughput RNA-sequencing data obtained from plant samples often contain sequences derived from novel RNA virus genomes, which can be identified by a comprehensive sequence analysis (Kim *et al.*, 2018; Koloniuk *et al.*, 2018; Orilio *et al.*, 2018; Park *et al.*, 2018; Zheng *et al.*, 2018). In this study, we analyzed high-throughput RNA-sequencing data acquired from a latex sample of the common fig (*Ficus carica*) and identified the genome sequences of two novel members of the genus *Closterovirus*.

*Corresponding author. E-mail: hahny@cau.ac.kr; phone: +82-2-820-5812.

Abbreviations: CP = coat protein; CPm = minor coat protein; CTV = citrus tristeza virus; FiVA = fig virus A; FiVB = fig virus B; FMMaV = fig mild mottle-associated virus; Hsp70h = heat shock protein 70 homolog; Hsp90h = heat shock protein 90 homolog; NCBI = National Center for Biotechnology Information; ORF = open reading frame; p6 = 6-kDa protein; RdRp = RNA-dependent RNA polymerase; SRA = Sequence Read Archive

Table 1. ORFs of the FiVA and FiVB genome sequences

ORF	FiVA (aa) ^a	FiVB (aa) ^a	Gene	Protein	Identity ^b	Pfam domain ^c
ORF1a	2956	2688	Polyprotein	polyprotein 1a	1399/2977 (47.0%)	Beet yellows virus-type papain-like endopeptidase C42 (PF05533), viral methyltransferase (PF01660), viral (Superfamily 1) RNA helicase (PF01443)
ORF1b	538	529	RdRp	RNA-dependent RNA polymerase	371/539 (68.8%)	RNA dependent RNA polymerase (PF00978)
ORF2	102	103		hypothetical protein	29/103 (28.2%)	
ORF3	215	204		hypothetical protein	84/216 (38.9%)	
ORF4	61	60	p6	p6 protein	48/61 (78.7%)	Citrus tristeza virus 6-kDa protein (PF06706)
ORF5	594	591	Hsp70h	heat shock 70-like protein	334/595 (56.1%)	Hsp70 protein (PF00012)
ORF6	507	524	Hsp90h	heat shock 90-like protein	241/525 (45.9%)	Viral heat shock protein Hsp90 homologue (PF03225)
ORF7	232	230	CPm	minor coat protein	145/233 (62.2%)	Closterovirus coat protein (PF01785)
ORF8	236	248	CP	coat protein	145/248 (58.5%)	Closterovirus coat protein (PF01785)
ORF9	58	58		hypothetical protein	20/58 (34.5%)	
ORF10	77	77		hypothetical protein	43/79 (54.4%)	
ORF11	187	189		hypothetical protein	51/189 (27.0%)	
ORF12	247	230	p28/p26 ^d	p28/p26 protein	102/252 (40.5%)	
ORF13	207	207	p23	RNA silencing suppressor	145/207 (70.0%)	RNA silencing suppressor P21 C-terminal domain (PF11479)

^aProtein length; ^bProtein sequence identity between FiVA and FiVB orthologs in the format: "Identical residues/aligned length (% identity)"; ^cPfam domain name and accession number; ^dORF12 encodes a 28 (FiVA) or 26 (FiVB) kDa protein.

Materials and Methods

A high-throughput RNA-sequencing dataset (3.5 Gbp) obtained from a latex sample exuded from the lignified trunk of a fig tree was analyzed with permission of the original author (Dr. Sakihito Kitajima, personal communication) (Kitajima *et al.*, 2018). The sequence dataset is available in the Sequence Read Archive (SRA) of the National Center for Biotechnology Information (NCBI) (Acc. No. DRR101542). High-quality reads were extracted using the Sickle program (version 1.33; <https://github.com/najoshi/sickle>) using the parameter "-q 30 -l 50", and then assembled into contigs using the SPAdes Genome Assembler (version 3.13.1; <http://cab.spbu.ru/software/spades>) using the parameter "--rna" (Bankevich *et al.*, 2012).

A total of 2,539 known RdRp domain sequences were extracted from 22 Pfam families (release 32.0; <https://pfam.xfam.org>) and converted to a BLAST-searchable database. Assembled fig transcriptome contigs were compared with known viral RdRp domain sequences using the stand-alone BLASTX program to identify putative viral genome contigs. The BLAST web server at the NCBI (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) was used for sequence similarity searches of viral genomes and proteins. ORFs were predicted using the getorf program of the EMBOSS

package (<http://emboss.sourceforge.net>), with the parameter "-find 1 -minsize 150 -noreverse". ORFs were identified based on sequence similarity to known proteins. Molecular weight of a protein was calculated using the pepstats program of the EMBOSS package. The HMMER web server was used to predict Pfam domains of viral proteins (version 2.40.0; <https://www.ebi.ac.uk/Tools/hmmer>).

Pairwise identities of protein sequences were calculated using the FASTA or GGSEARCH programs in the FASTA package (version 36.3.8g; <https://github.com/wrpearson/fasta36>). Multiple sequence alignments were generated using the MAFFT program (version 7.450; <https://mafft.cbrc.jp/alignment/software>) with the parameter "--auto" (Nakamura *et al.*, 2018). Maximum likelihood phylogenetic trees were inferred using the IQ-TREE program (version 1.6.12; <http://www.iqtree.org>) with the parameter "-bb 1000" (Nguyen *et al.*, 2015).

Results and Discussion

Two different contigs (19,333 bp and 18,741 bp) derived from fig RNA sequencing data were identified to have an ORF showing a high sequence similarity to the citrus

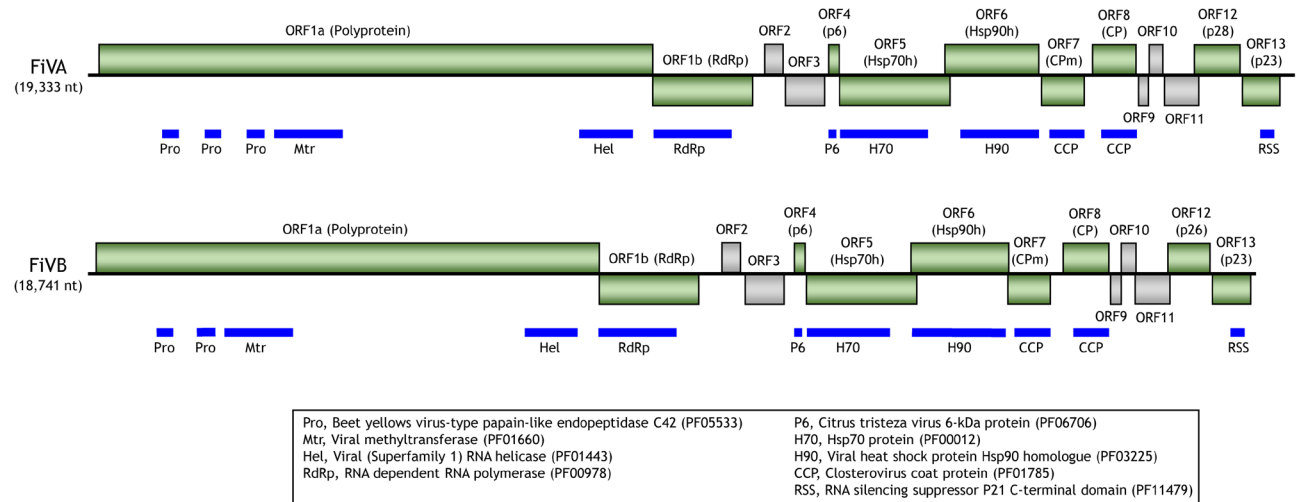


Fig. 1

Genome structures of FiVA and FiVB

Predicted ORFs are represented by boxes: green, ORFs with homologs in other closteroviruses; gray, ORFs present only in FiVA and FiVB. Predicted Pfam domains are marked by blue lines below the ORFs, and their names (as listed in the Pfam database) are shown in the box at the bottom.

tristeza virus (CTV) RdRp domain sequence. CTV is one of the approved species of the genus *Closterovirus* from the family *Closteroviridae* (Karasev *et al.*, 1995). BLASTX searches of these contigs against the NCBI protein database confirmed that they contained ORFs having similarities to those of known closteroviruses. Therefore, the two contigs were considered distinct novel closteroviruses and named fig virus A (FiVA) and fig virus B (FiVB). Their nucleotide sequences were deposited in the NCBI nucleotide database under the accession numbers MN817232 and MN817233 for FiVA and FiVB, respectively.

In the FiVA and FiVB genomes, ORFs encoding 50 aa or longer were initially predicted. Following this, orthologous pairs of ORFs showing significant protein sequence similarity (an E value of 0.001 or less using the FASTA program) were selected. As a result, a total of 14 ORFs (ORF1a, ORF1b, and ORF2 to ORF13) were predicted in each genome (Fig. 1 and Table 1). Pairwise protein sequence identities of respective orthologs ranged from 27.0% to 78.7%. Sequence alignments of 14 proteins with their respective orthologs from other members of the family *Closteroviridae*, if any, are presented in Supplementary Figs. S1a, S1b, and S2 to S13. Nine ORFs (ORF1a, ORF1b, ORF4, ORF5, ORF6, ORF7, ORF8, ORF12, and ORF13) had orthologous proteins annotated in other members of the family *Closteroviridae*, whereas five ORFs (ORF2, ORF3, ORF9, ORF10, and ORF11) were predicted to be present in FiVA and FiVB, but showed no significant similarities to known proteins.

Polyprotein (ORF1a) and RdRp (ORF1b) are present in all members of the family *Closteroviridae* (Fuchs *et*

al., 2020). Polyproteins encoded by FiVA and FiVB ORF1a were 2956 and 2688 aa, respectively, and contained three functional domains: papain-like protease, methyltransferase, and helicase. Interestingly, the FiVA polyprotein had three papain-like protease domains, whereas the FiVB polyprotein had two, which made the FiVA polyprotein longer. The closterovirus RdRp domain is produced by +1 ribosomal frameshifting, resulting in the fusion of ORF1a and ORF1b to ORF1ab (Agranovsky, 2016). The ribosomal frameshifting usually occurs at the ORF1a stop codon preceded by two uridines (Orilio *et al.*, 2018). The potential ribosomal frameshifting sites of FiVA and FiVB were `cgcGUUUAGCugg` and `cgtGUUUAGCuc`, respectively, where the conserved stretch in two viruses is indicated by uppercase letters, stop codons (UAG) of ORF1a are in bold, and putative first codons (AGC) of ORF1b are underlined.

The ORF4 sequences of FiVA and FiVB were predicted to encode 6-kDa proteins with a domain conserved in p6 proteins of some closteroviruses including fig mild mottle-associated virus (FMMAV), rose leaf rosette associated virus (RLRaV), CTV, mint virus 1 (MV-1), and BYV. The p6 protein is one of five proteins (p6, Hsp70h, Hsp90h, CPm, and CP) involved in cell-to-cell movement (Peremyslov *et al.*, 2004). All seven analyzed p6 proteins were predicted to have a transmembrane domain that plays an important role in cell-to-cell movement (see Supplementary Fig. S4).

ORF5 and ORF6 of FiVA and FiVB encoded the heat shock protein homologs Hsp70h and Hsp90h, respectively. Two coat proteins (CPm and CP) were predicted to be

Table 2. Sequence identities of the Hsp70h and RdRp proteins of FiVA and FiVB and their respective orthologs

No.	Genus	Virus	Acronym	NCBI ^a	FiVA Hsp70h	FiVB Hsp70h	FiVA RdRp	FiVB RdRp
1	<i>Closterovirus</i>	fig mild mottle-associated virus	FMMaV	FJ611959	217/600 (36.2%) ^b	221/597 (37.0%)	147/285 (51.6%) ^c	137/276 (49.6%) ^c
2		raspberry leaf mottle virus	RLMV	NC_008585	222/612 (36.3%)	224/608 (36.8%)	265/538 (49.3%)	275/529 (52.0%)
3		rose leaf rosette-associated virus	RLRaV	NC_024906	216/606 (35.6%)	206/602 (34.2%)	261/539 (48.4%)	267/531 (50.3%)
4		Citrus tristeza virus	CTV	NC_001661	202/604 (33.4%)	211/608 (34.7%)	279/539 (51.8%)	276/529 (52.2%)
5		strawberry chlorotic fleck-associated virus	SCFaV	NC_008366	216/608 (35.5%)	198/600 (33.0%)	267/538 (49.6%)	274/529 (51.8%)
6		carrot yellow leaf virus	CYLV	NC_013007	215/625 (34.4%)	214/618 (34.6%)	242/540 (44.8%)	242/531 (45.6%)
7		carnation necrotic fleck virus	CNFV	NC_038419	182/611 (29.8%)	177/611 (29.0%)	246/539 (45.6%)	247/530 (46.6%)
8		mint virus 1	MV-1	NC_006944	207/611 (33.9%)	199/610 (32.6%)	246/539 (45.6%)	252/530 (47.5%)
9		tobacco virus 1	TV-1	NC_027712	196/612 (32.0%)	196/610 (32.1%)	250/541 (46.2%)	254/530 (47.9%)
10		Rehmannia virus 1	ReV-1	NC_040572	185/612 (30.2%)	195/611 (31.9%)	254/539 (47.1%)	255/530 (48.1%)
11		beet yellows virus	BYV	NC_001598	195/605 (32.2%)	208/602 (34.6%)	252/538 (46.8%)	253/529 (47.8%)
12		arracacha virus 1	AV-1	NC_040570	193/609 (31.7%)	196/606 (32.3%)	248/538 (46.1%)	255/530 (48.1%)
13		beet yellow stunt virus	BYSV	NC_043106	205/620 (33.1%)	213/616 (34.6%)	256/542 (47.2%)	253/531 (47.6%)
14		grapevine leafroll-associated virus 2	GLRaV-2	NC_007448	201/616 (32.6%)	199/608 (32.7%)	246/538 (45.7%)	248/529 (46.9%)
15		blackcurrant leafroll-associated virus 1	BcLRaV-1	NC_040722	192/609 (31.5%)	201/605 (33.2%)	247/538 (45.9%)	249/530 (47.0%)
16	<i>Unassigned</i>	blueberry virus A	BVA	NC_018519	166/625 (26.6%)	178/624 (28.5%)	221/539 (41.0%)	231/532 (43.4%)
17		Actinidia virus 1	AcV-1	NC_035453	185/613 (30.2%)	167/607 (27.5%)	182/574 (31.7%)	189/561 (33.7%)
18		persimmon virus B	PeVB	NC_025967	179/613 (29.2%)	172/610 (28.2%)	190/541 (35.1%)	192/539 (35.6%)
19	<i>Velarivirus</i>	Areca palm velarivirus 1	ArPV-1	NC_027121	166/608 (27.3%)	171/614 (27.9%)	151/549 (27.5%)	147/536 (27.4%)
20		Cordyline virus 1	CoV-1	NC_038421	152/602 (25.2%)	155/599 (25.9%)	137/547 (25.0%)	136/537 (25.3%)
21	<i>Crinivirus</i>	lettuce chlorosis virus	LCV	NC_012909, NC_012910	177/605 (29.3%)	170/612 (27.8%)	130/547 (23.8%)	131/537 (24.4%)
22		lettuce infectious yellows virus	LIYV	NC_003617, NC_003618	165/604 (27.3%)	170/604 (28.1%)	145/543 (26.7%)	148/536 (27.6%)
23	<i>Ampelovirus</i>	grapevine leafroll-associated virus 1	GLRaV-1	NC_016509	156/606 (25.7%)	147/603 (24.4%)	154/540 (28.5%)	153/532 (28.8%)
24		grapevine leafroll-associated virus 4	GLRaV-4	NC_016416	161/611 (26.4%)	150/602 (24.9%)	158/542 (29.2%)	159/536 (29.7%)

^aNCBI Acc. No. for genomic sequence; ^bAmino acid sequence identity in the format; “Identical residues/aligned length (% identity)”;
^cFMMaV RdRp is partial.

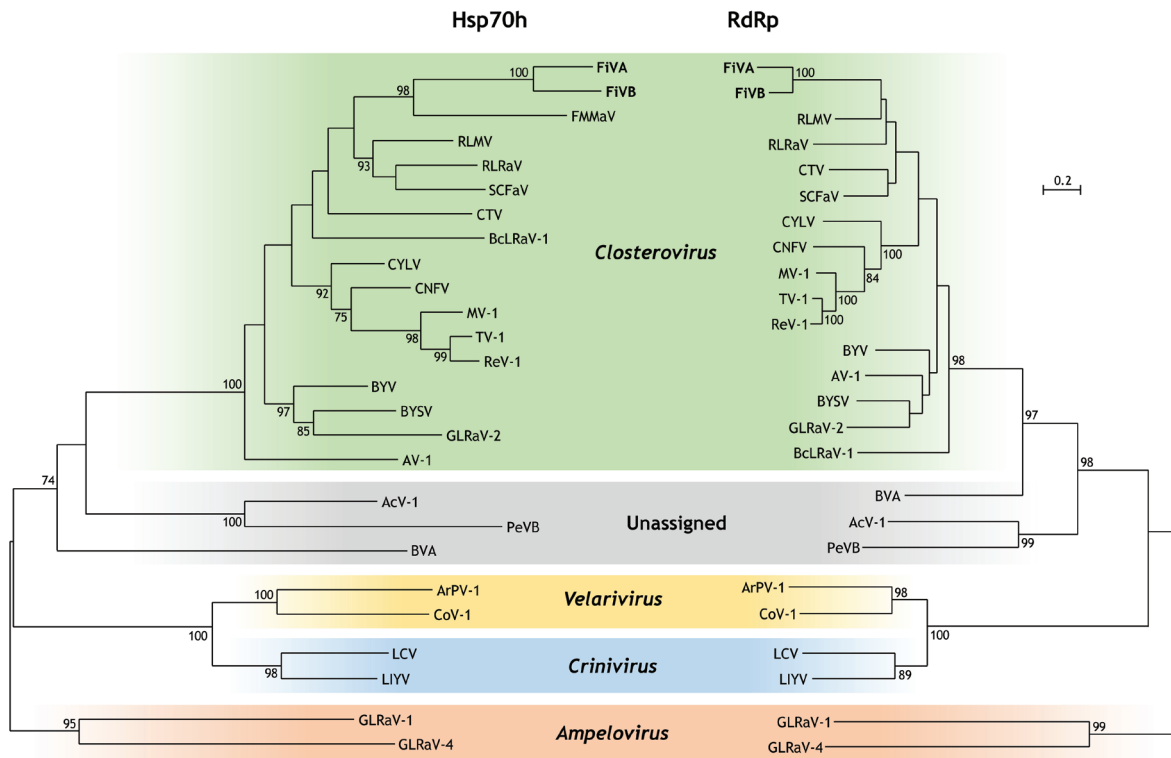


Fig. 2

Phylogenetic trees inferred based on Hsp70h (left) and RdRp (right) protein sequences of FiVA, FiVB, and selected members of the family *Closteroviridae*

Note that FiVA and FiVB form a subclade within the genus *Closterovirus*. The FMMAV RdRp, which is partial, was not included in the RdRp tree. Bootstrap branch support values of 70% or greater, calculated from 1,000 replicates, are shown at the nodes. See Table 2 for the full names of viruses and their NCBI Acc. Nos.

encoded by ORF7 and ORF8, respectively, of the FiVA and FiVB genomes. Hsp70h, Hsp90h, and CPM were known to be involved in vector transmission (Killiny *et al.*, 2016). They showed strong sequence similarities to respective orthologs of members of the family *Closteroviridae*.

The ORF12 proteins of the FiVA and FiVB genomes showed sequence similarities to the 29-kDa protein (p29) of three persimmon virus B (PeVB) variants, the function of which was not known (Ito *et al.*, 2015). The FiVA and FiVB ORF12 proteins were named p28 and p26, respectively, according to their calculated molecular weights. All five proteins from FiVA, FiVB, and three PeVB variants were predicted to have a signal peptide at their N-termini (see Supplementary Fig. S12).

ORF13, which is the last ORF of FiVA and FiVB, encoded a 23-kDa protein, which showed a similarity to the CTV p23 protein. The FiVA and FiVB p23 proteins were predicted to have an RNA-silencing suppressor domain, which is also found in p23 orthologs of some closteroviruses, including the CTV p23, BYV p21, and grapevine leafroll-associated virus 2 (GLRaV-2) p24. One of the functions

of p23 orthologs is the intracellular suppression of RNA silencing (Flores *et al.*, 2013).

Five ORFs (ORF2, ORF3, ORF9, ORF10, and ORF13) had no homologous protein sequences in the current NCBI protein database. Hypothetical proteins encoded by ORF3, ORF9, and ORF10 were predicted to have a transmembrane domain near the C-terminus (ORF3) or in the N-terminal region (ORF9 and ORF10) (see Supplementary Figs. S3, S9, and S10, respectively).

Phylogenetic positions of FiVA and FiVB were determined using Hsp70h and RdRp sequences. A total of 24 sequences from representative members of the family *Closteroviridae* were collected (Table 2). FiVA and FiVB Hsp70h showed 24.4–37.0% sequence identities to Hsp70h proteins of selected viruses. Sequence identities between the FiVA and FiVB proteins were 56.1% (Hsp70h) and 68.8% (RdRp), suggesting that FiVA and FiVB are closer to each other than to other known closteroviruses. The RdRp of FiVA and FiVB showed 23.8–52.2% identities to the RdRp sequences of selected viruses. Conserved Hsp70h domain and RdRp domain sequences were extracted from respec-

tive multiple sequence alignments (see Supplementary Figs. S1b and S5) and separately subjected to analysis using the construction of phylogenetic trees.

The Hsp70h and RdRp phylogenetic trees confirmed that FiVA and FiVB are novel members of the genus *Closterovirus* in the family *Closteroviridae* (Fig. 2). In both trees, FiVA and FiVB formed a strong subclade with a bootstrap support value of 100%, indicating that they are the closest among the analyzed closteroviruses. The next closest virus to FiVA/FiVB was FMMAV, another closterovirus infecting figs (Elbeaino *et al.*, 2010). These three viruses formed a subclade, which was supported by a bootstrap value of 98%, in the Hsp70h tree. Therefore, FiVA, FiVB, and FMMAV could be descendants of a common ancestral closterovirus that infected figs in the past, though they may have a complex history and simply were identified in figs. No ancestral nodes of the FiVA/FiVB/FMMAV clade had a bootstrap value of 70% or greater except for the node of the genus *Closterovirus* (100% and 98% for the Hsp70h and RdRp trees, respectively), indicating that the phylogenetic positions of three fig closteroviruses within the genus *Closterovirus* cannot be unambiguously determined.

To conclude, genome sequences of two closteroviruses, FiVA and FiVB, were identified by high-throughput RNA sequencing from a fig latex sample. Phylogenetic analysis confirmed that FiVA and FiVB are novel members of the genus *Closterovirus* in the family *Closteroviridae*. FiVA and FiVB genome sequences are useful resources to investigate the evolution of closterovirus genome organization.

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Supplementary information is available in the online version of the paper.

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Dongbin Park, Chul Jun Goh, Yoonsoo Hahn*

Department of Life Science, Chung-Ang University, 84 Heukseok-ro, Dongjak-gu, Seoul 06974, Republic of Korea

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Keywords: fig virus A; fig virus B; Closterovirus; common fig; *Ficus carica*

*Corresponding author. E-mail: hahny@cau.ac.kr; phone: +82-2-820-5812.

Fig. S1a. Alignment of polyprotein (ORF1a) sequences of FiVa, FiVb, and related viruses

FiVa	-----M-----	SKVPSFFPNPI	-----PRVK-----	I-REKYFLFFKGPLTAADTP-GRVA--	-----HRRRFVVKM-----	48					
FiVb	-----M-----	TSVSFMLPPD	-----PDIT-----	I-IRSRAPPTSPLKGLLKP-SPPI-	-----PRRSSLPPF-----	48					
RLMv					-----MSP-----	4					
RLRaV	M-----	KTFYV	FADDPDPL		PVPGS-----	PVPPINPPFVDHA	33				
SCFaV		MAGS	HNHPWF		IG-----	YSPG	17				
CTV						MSKL	4				
BcLRaV-1		MA	SVSPMIAC		PSDAE	LLEL	19				
CYLV		MAIVS	TQVQTHF		AAS	FDQT	19				
CNFV		MSAIV	PFVPVQLL		FHGGASH	VRNV	25				
MV-1		MAVCV	FAVPIFS		SGN	LSVP	19				
TV-1		MVLSI	FVVPFS		VAD	LNSP	19				
ReV-1		MALAV	FAVPVFT		IGN	LLEP	19				
BYV		MAFLN	VSAPVSCAFAPA	FA		SPTV	28				
GLRaV-2	M-----	SSLAI	STLPCSVAQLS		FGQPVAAV		25				
AV-1		MAFLVDS	SMSPSASL			FNKQV	20				
AcV-1	MAPPFRFLKASSGRAKASVAS		RLNTRGECCKTLPKGWNSSFTVAHF	FGAEDREVTF	SRGCSRIDAYGLNPPPAV	FGPEPASPAFLKARANRELYSGVQRPFNSRK	108				
BVA						MY	2				
PeVb	MK-----	RGSNGRCYEAVLRS	AEDYLMR	-----MTGPHGRYASL-----	RS-----	AVKSPPSLGQWPLASDVALA	-----LSGMFAPF-----	64			
ArPV-1								0			
CoV-1		MAFRS		SPLI				9			
LCV		MAVMS		HSLQLNDCVW		PLVGP	ALDSAC	26			
LIYV		MALEV		ES				7			
GLRaV-1		MAVKS		IFAQE		DLISTQKD	FRFPFVSS	26			
GLRaV-4				MPRPGFSDDP		PLAAP		16			
FiVa		CQSLYKA-TLA				LPH	61				
FiVb		LQSLYRA-PLA				LPH	61				
RLMv		FGELLVE-V-ATDPE		TLRYLEAVHAAEA	KAKLPTNLCRDIV	LSLP-V	48				
RLRaV	AIAWYMGFEYRPHFYRA					KN	54				
SCFaV		SGSFIKT		HLAPVYVYDGGTLLSKL			41				
CTV		RGSFWSS-AIAVNSDYTISRWRKL	NTIIVLHYFGFVRI	TKV-----	IRDKS-----	ADMPIV	56				
BcLRaV-1		EAEYLRSKALAAKPPSNEDPLS		ALCDRITTFQREAAKDAV		QSAA-LSACALTVWETRHV	76				
CYLV		FNAFLSA-ATFTSPSF		YRLSVSQTLSKIDKLSKNKV		LVT-IS	60				
CNFV		FNSISRS-CAGVSAQK		RFALFTRL-CAPFTFNVTYVLTKDYI		LCF-V	69				
MV-1		RLSFEIA-PATAVPG		LSQLTFMSDCTGKEIV		LST-V	54				
TV-1		VASFVYS-AYGVVPA		NAVKVDFDPVAVTSADDA		GCI-V	54				
ReV-1		EVSFVFS-AFGVVPT		GACRAFDLPACYSADSE		GAI-V	54				
BYV		PDSFPCV	PRYSDDISHFLR		TLSDFSVPRPLSLNAR	VH	LSASTDN	73			
GLRaV-2		AKSFLMT		SL				34			
AV-1		ATSLVVS-MLAS				MSLF	IAGSVDS	42			
AcV-1	AVRQA	---AVAASLFEA	RR		QRASKVHLPVVGKRRKAGPAFKAPKDDVQHTTIPV	VAPTVPVVP	TTFP-VAYVAKGATRL	185			
BVA		QHTFQRA-AARMSYQRSLNQ			THIRRTLRTRVVDSEGF	TSF	VREHC	46			
PeVb		PVGLFFA			WLSRTSYR		VAHVTSASHVCRSWQTR	97			
ArPV-1						MSNGRS		6			
CoV-1			KRKQTKQT		NHNQTSLNHRKRVKK		MKNLRKTKEY	42			
LCV		VPQLWSAGAVSCSPKNPNNNN			NNKNQKWLKNKQTR		LGHVKTSEVS	72			
LIYV		AFSLSYLLKENKQT			SNLFLSLIQVPYTK		MTHAKGKKTTH	45			
GLRaV-1		STSLFLC	NL					35			
GLRaV-4		SHSSFPNP			TAHQWIPKTTYKNNTS		V-----ISGSTAHRTRKAEQERAO	61			
FiVa	--PSVGV----	SPRI		RGVPGHIPG		TRFLPETV	YATPCGSTRPRPASLRAVLAAR	110			
FiVb	--PNQGV----	SPRI		RGVPGVVP		SRTLRLVL	YADASGICRPRAQSLRAL	106			
RLMv	--PIRER----	RPR		PLPH		VF	CVNSAGVCSPLNER	76			
RLRaV		FPR					QIFISSAGAI	SPYSES	73		
SCFaV	--PVRTD----	RP				CTTAS	-----ISSK	57			
CTV	--PLRKS----	VFPF		SVRAAVTSFVLLG		VLLTL	RIQGASVAFPLSTHLALFVP	103			
BcLRaV-1	--NRLRRP----	TPD		SQHRESLRR			RRSLCEGQQRTRDLSLRASP	115			
CYLV	--PSKNF----	S				FLF	QLPSPISSSLRHYPRKREP	89			
CNFV	--AVRRI----	SPS		AGVMIAVRR				86			
MV-1	--PSTGV----	APSC		TPSTLAKRRSILRRPTH		LPKGECTFYCG	LTEGTAHRSPRRDIGKSF-P	110			
TV-1	--PV-----			GTRATDGS		HCV	RQPTSGEVKVPRHCGGV	84			
ReV-1	--PVSAT----	G		DGVAR		CP	LLKASVASKVPFVSNRS	84			
BYV	--PLPST----			PLGFHA		ETF	VLELNGSSAP	97			
GLRaV-2	--PSLQT----	YPSLSELT	SFSF		CFGVFNQKMFMSFLRS	---VHVFASFSELSTFGSCYEFIRLGGGAHL		97			
AV-1	--GPLMSLISL	CLSKVLKEGLRL			TDGYTASAT			S	75		
AcV-1	--PEGTPVFLAKKPAARTLGFYPK			RAQREFIRLSLDGWSVTLDTESGVVTDQALLTLVKNYHYEAF	LPKLLAKHGAKLTP	LEYGMVRYDRNGRISRLNLNLPYMW		289			
BVA	--PVRPT----	TSPRNFRPAPRNP	PAYAHGNRSAGVP	SGGTS	SSHSPR		RPSGSAFVPPSGGARFVPA		111		
PeVb	FGPVRAL	TDMAKVPNVRVGGYSP		RRDSRCLSLGLAAAVHTLL			LTEGRRREADVISYGRQV	---G	164		
ArPV-1									6		
CoV-1	--KISKI----	NNKITSI			TSALIEQRRRVY		IHEDTLPDPPKSDKDWEIFS		87		
LCV	--PASCV----	RSKVAF			RRR				86		
LIYV	--LLRCI----	LG							52		
GLRaV-1	--PSPPI----						IFQKGSRFIAPTRSSNGFLRKAID		64		
GLRaV-4	--GPOSKF	SNLTVKGAALKGKQ					ATDQRPKPSNKELATV		100		
FiVa	-----LAARKL-----	R-FAASTN				RTRFRSRK		131			
FiVb	-----LRDRRL-----	R				RCRAPRRA		121			
RLMv		FLSSSR				RRIVKR		88			
RLRaV		FRQASR				RRARSERVARKSLKE		94			
SCFaV		MLGASR				AAKLNS		69			
CTV		ALFAGFSR				FSLCKP		117			
BcLRaV-1		FAEMAK				RCSLQS		127			
CYLV		CVFYAQDG				TIES		101			
CNFV		DATSPG				VIIIT		96			
MV-1		CLFVASGG				ICHKV		123			
TV-1		FTKSGAS				ARSCVAKDS		100			
ReV-1		HTPSYGP				WFKVWISS		100			
BYV		FSPSRHDF				VVNR		111			
GLRaV-2		FFCSFO				CG		105			
AV-1		FRRVPR				ATRKLRSLSLTH		102			
AcV-1	---EVLQLL	KRGECPKLRAYIES	FQDMRGYCYL	KFRMANIAIGRSARRVGT	VCHILG	SFSPSTREVQTVLYRRYACIPDF	IVGYSQGRGHMTT	TPPIVRVSALPDLWYGDCL	401		
BVA		SPGRR				FVDSRG		VAHRHF	FNN	132	
PeVb	GPSDAAN	LVQEGRADSG	GATALHFC	CRGCGCRM	VFSVPR	PACAKCGGRVSVSS		LMRREAPKPR	VSGLKKKATSADGWTT	-----FYRERD	249
ArPV-1						YASGTGGLCW		VNAFAYY	NVNI		27
CoV-1		RFN				MVHYTDMGHNF		VGDEHY	YIMP		114
LCV						LVS					89
LIYV											52
GLRaV-1						YAVCCKN	YGRSL				76
GLRaV-4						YRSCGR	VL	SY			110

FiVa	----	PLAS	-----	SVSPS	-----	LKSP	-----	145
FiVb	----	PPAA	-----	PRGQ	-----	KKSP	-----	133
RLMV	----	PSVP	-----	SESTGVLPA	-----		-----	102
RLRaV	----	PRVA	-----	SPGVKAP	-----	FAQDP	-----	110
SCFaV	----	GVGP	-----	RRTP	-----		-----	77
CTV	----	PLT	-----		-----		-----	120
BcLRaV-1	----	PRSV	-----	ACDFSSTGTI	-----	TRDASSHSPL	-----	152
CYLV	----	PVSR	-----	HTAPS	-----		-----	110
CNFV	----	PITS	-----	RLPSEGKRTG	-----	NRYDTMCSQP	-----	122
MV-1	----	PFTP	-----	ENVNTSCLFV	-----	RODGRCSKVP	-----	147
TV-1	----	PVSS	-----	RRTPRGMYA	-----	RTDGLKASSP	-----	124
ReV-1	----	PVIS	-----	DTSPNRVLYA	-----	KVDGTIKDSP	-----	124
BYV	----	PFSV	-----	FPTVELSVSSLRTPSRLFALLCDFLYCSKPG	-----	PCVEIASFSTPPCLV	-----	163
GLRaV-2	----	PLSVSLGLVGVFAVLNLSFPLSNASLLMDVGKDVQVKRKIKLEKKQKRVS	-----		-----	MARAARYVPS	-----	173
AV-1	----	PKSFL	-----	GKGNFYADKNCCCVF	-----	SWSSIEY	-----	140
AcV-1	MFGSIPASI		-----	PVKAITSSPLKPGCS	-----		-----	450
BVA	----	PRPAS	-----	GSAAFRAW	-----	PP	-----	155
PeVb	----	NSSPRS	-----	RSEPVRAIRAPQPKRCA	-----	S	-----	319
ArPV-1	----	P	-----		-----		-----	28
CoV-1	----	PATD	-----		-----	G	-----	119
LCV	----	P	-----		-----		-----	90
LIYV	----		-----		-----		-----	52
GLRaV-1	KFDATPVQS		-----	THHIIVKAVFRNTYIRAAS	-----	GKMWTLR	-----	111
GLRaV-4	----	NSKIPASA	-----	PRPNGVSASSSPKSYTSS	-----	SCSYHSSLSSGPKY	-----	151

FiVa	----		-----	RQHKTDL	-----	NDYKKS	-----	158
FiVb	----		-----	KVNKTIINNDAKRS	-----		-----	147
RLMV	----	SSASFRNALREA	-----	GVSVPSTFFSFPASAGQL	-----	VLVRAALKSPKQNNRKL	-----	185
RLRaV	----		-----		-----	LLITNYGLLLVRGDGASFSR	-----	121
SCFaV	----	AKVRRS	-----	QVPEWILNHSSVAFDNL	-----	KIFFKTISKPKQNNPYNT	-----	153
CTV	----	SAAKRSLR	-----	QAKRESVLSRASSR	-----	FSEVPRGTRSLH	-----	197
BcLRaV-1	----		-----	TFSASADDDITF	-----	ANMYLNLKSLCLVNAKRE	-----	222
CYLV	----	SEKEARKV	-----	FDTRKFNHQ	-----	NKTKIMILSHDRGD	-----	161
CNFV	----	SVGSLSVSEH	-----	TKVSIKSFDLKAQFNHR	-----	NKTKIITINRQTD	-----	187
MV-1	----	CP	-----	TARRSD	-----	ATVGKGGFSLTRQFNHR	-----	210
TV-1	----	SRQARQDV	-----	VIGDGHGFSLNKQFHDR	-----	TRTKAMIINHDGD	-----	188
ReV-1	----	SKCPVRRNV	-----	TIGGPHGFDVTRQFHDR	-----	KHSTKMIINPNSGD	-----	188
BYV	----	SNCAQIPIHAEEMESIRFPTKTLPAGRFLQHFHRKYT	-----		-----	KRPELTIHESGLAL	-----	238
GLRaV-2	----	RNPKEKRAVHVQPLP	-----		-----	SGSFRFSQDK	-----	244
AV-1	----	DLAMSLRLVQVSTLEVSRCFEVSYGTFVYRVFKTFVCAF	-----		-----	NKVSFTV	-----	190
AcV-1	EKPSVAMSKSAIRLRKNAAH	----	----	RAGVH	----	----	----	529
BVA	----	SPTVIRRSSGASAE	-----	AATIRTPPF	-----		-----	188
PeVb	----	RKGAVSGSPSVIRDLPRFAPVR	-----	GARV	-----	VRAPVSRCPKREIIPPVRGGLE	-----	369
ArPV-1	----		-----		-----	KTLPF	-----	48
CoV-1	----		-----	HYVNVTTVND	-----	STLKVLFKARQCFSKAVLNRIQLEL	-----	158
LCV	----		-----	GI	-----	SPVEIQILSNGNALVQP	-----	116
LIYV	----		-----		-----	SPFETL	-----	64
GLRaV-1	----	AGTASGTVRLVRPAVV	-----		-----		-----	127
GLRaV-4	----	SRPHEYTLSDVQALVQHNVT	-----		-----	PHVQAVKLSRPNGI	-----	186

FiVa	----		-----	VPFTPN	-----	PLKYAPMRAKPT	-----	176
FiVb	----		-----	YDILTGV	-----	IPDRYRVATRPR	-----	167
RLMV	STTVYISGKN	----	----	RRARVRGDA	----	----	----	234
RLRaV	ISSEFVDPISNGERKGSPLNYTM	----	----	SPAARP	----	----	----	178
SCFaV	PVVFCSRRM	----	----	RKTPTQTECN	----	SV	----	206
CTV	LDLIL	----	----	RWIEEENPHP	----	SM	----	225
BcLRaV-1	FCLSLHS	----	----		-----	KGSSAFSGGGCNTARK	-----	265
CYLV	HYRTLACAPR	----	----	ERXASHRRK	-----		-----	218
CNFV	CLVTFFS	----	----		-----	THVPFRKSAADRKKK	-----	224
MV-1	RRISLFS	----	----		-----	KPFTA	-----	231
TV-1	GAYNLR	----	----		-----	TPFVR	-----	210
ReV-1	GAYLRS	----	----		-----	TPFSRKNF	-----	211
BYV	EKYEAYE	----	----		-----	ISRKD	-----	266
GLRaV-2	VKFRCA	----	----		-----	PSCSTSACLKRIIVRVA	-----	294
AV-1	----	----	----		-----	GTPYSPPESTNLKRT	-----	223
AcV-1	GLRL	----	----	SWFGKVNPNERNKDRLASLLSADGSGYNYNGGSHRPPDKRSKTL	-----	LAELESLSLIDL	-----	636
BVA	----	----	----	PST	-----	PSEVAVPFYVDRNRLTQA	-----	227
PeVb	----	----	----	RVDDVVK	-----	PLYSAWVPVGGVITERP	-----	425
ArPV-1	----	----	----		-----	VNFLR	-----	55
CoV-1	----	----	----		-----	TKPQIKYLKK	-----	184
LCV	----	----	----		-----	TRLDMLRKCINCP	-----	136
LIYV	----	----	----		-----	RLKLNREVCLNP	-----	84
GLRaV-1	----	----	----	ELES	-----	DHAGMFSVFVRKQ	-----	161
GLRaV-4	----	----	----		-----	YPRTPQKVMFKGQEVSSPQGLNSSPVRA	-----	GP 234

FiVa	----	KPWVGKPRTCQ	-----		-----	YDDVPTTLPLGVSAPPVV	-----	219
FiVb	----	KQWRGKPLTSL	-----		-----	WDVCETSPQMPETALEIVP	-----	211
RLMV	----	TPRTAA	-----		-----	YHACPSVEVRTAFNDT	-----	268
RLRaV	----	TERTAA	-----		-----	WRNAEECTQRTSYNPI	-----	209
SCFaV	----	TPKTA	-----		-----	YHNSPVCETRYND	-----	234
CTV	----	MPATAW	-----		-----	CSHSEAAVLRAALIT	-----	279
BcLRaV-1	----	VRKTPSPFKPSAA	-----		-----	WHLVDASDHTRTFNAGE	-----	295
CYLV	----	NPRKG	-----		-----	DAFKPKSRN	-----	240
CNFV	----	KPRTTF	-----		-----	NWNAFTFGSLHFVDG	-----	259
MV-1	----	TPRRTS	-----		-----	HRFRTPSPNEINTL	-----	267
TV-1	----	FNKIPRKS	-----		-----	VNIYTOPITEVNTLSV	-----	247
ReV-1	----	TPLSR	-----		-----	VKSTFVQQKNHINVLPI	-----	247
BYV	----	KPRKIN	-----		-----		-----	272
GLRaV-2	----	TPKVR	-----		-----	ENPAGAL EANSEASATS	-----	330
AV-1	----	IPRVFP	-----		-----	YTRNVRRKVTYTYAPPSTLNSIRIFGELMREDEPKIVPKAPASFIYVQGI	-----	286
AcV-1	SRGAERYNI	GLDGP	----	CMF	----	EDPDSVNFDFHDSVEVGRFRGSLITLRGHKSSNVL	----	735
BVA	----	AVPVSPPGSS	-----		-----	PTVSAATSHTSVSSVA	-----	264
PeVb	----	KKEVQALDPSASGRKEPVLFF	-----		-----	SQEPATPGQRYARSHGVLVYVKEEPLPADKDAGPS	-----	495
ArPV-1	----		-----		-----	RVVSNLLHFDNKYVQNAKIQH	-----	85
CoV-1	----	PKNVVYTY	-----		-----	KRHTDNHILNCAQGRDNKQVCG	-----	222
LCV	----	QAVINKLGYDVD	-----		-----	KINEDIDQALNSKVGTPENTRQPD	-----	181
LIYV	----	PKNISYKQNPFL	-----		-----	KLYEINNNFINCKVGTGNTNSTYDWRN	-----	129
GLRaV-1	----	RKPAQSKIPVPTIKAK	-----		-----		-----	178
GLRaV-4	----	SSGNVPKGGVQNPQSGG	-----		-----		-----	272

FiVa	-----PLTLVSRD-----	-----GSDFDVPSRGINPR-----	448
FiVB	-----FALITAAD-----	-----GTDFDVPAYGLINPR-----	435
RLMV	-----TGYAPPISW-----	-----F-PKGVEFEK--FKK-----	500
RLRaV	-----PPVRVHRIK-----	-----C-----	425
SCFaV	-----YKALPLESR-----	-----F-VKQAPVDEVDFKK-----	464
CTV	LKPSLGRIPSIDRRFRFPAGTQLRVSVPRRVDHVYVSTGSNFDELCHAVLTRMSKGTLEILLHSIRERKGLLGFACFRWSSSHVFKRGNF	-----TARFPISAVRYENQ-----	661
BcLRaV-1	-----SR-----	-----ASPFNETTTTYAGGK-----	515
CYLV	-----VP-----	-----F-----	275
CNFV	-----TPAPTR-----	-----SLTTEQYKRV-----	365
MV-1	-----QPS-TR-----	-----NFKLSAEKVNS-----	345
TV-1	-----VRGEMTLPKSKIRDL-----	-----VRGEMTLPKSKIRDL-----	323
ReV-1	-----SLPKRKLKSL-----	-----SLPKRKLKSL-----	321
BYV	-----HPILRSA-----	-----SYTFGFKMPLQRFMK-----	394
GLRaV-2	-----L-TSVITVKTSGLPDSRPKS-----	-----L-TSVITVKTSGLPDSRPKS-----	599
AV-1	-----GLDVSIVRTAATKHLRGRQY-----	-----GLDVSIVRTAATKHLRGRQY-----	1005
AcV-1	ERKECPKSPIRTNN	-----SMPALKALPVRRLSPLM-----	518
BVA	-----CGESPP-----	-----SSEELMRTRISKGLSPRAE-----	698
PeVB	-----IFLDTPIPTQO-----	-----PTTTRRLQOTPEPSGVQ-----	243
ArPV-1	KPAVVVNTTIPTNK	-----PTPIAITKVKDKPSFIQ-----	444
CoV-1	-----FMRSKVGVT-----	-----PEL-KVTQVPKKNNT-----	335
LCV	-----RFQTNIITP-----	-----VKP-RVSVNKAREV-----	273
LIYV	-----VPLEVIR-----	-----Y-----	268
GLRaV-1	-----F-----	-----F-----	358
GLRaV-4	-----F-----	-----F-----	358

FiVa	LLFAAFN-DV-----PSFPRKRS-----VRRAYLSEGNLTKSL-----	-----DYIVR-----	485
FiVB	LSFAAFG-AV-----SPFRGHRY-----	-----VRTTHLHEKDLVRL-----	472
RLMV	-----DI-----PFDLGK-----	-----DNTFYLRADDLPTAL-----	529
RLRaV	-----DS--DY--PSDCPPT-----	-----WESFYFRGKVSRRV-----	456
SCFaV	-----A-----PF-----	-----TGVLPVTKLDAVV-----	485
CTV	--YAAMMDV-----GTSWPKGYVPDQVVKRRRS--RNRFPPLSHRAVDQSV-----	-----PALQSSPVEVASVSSDKPSSS-----	727
BcLRaV-1	-----SYNLGGEQLAK-----LPQPRN-----	-----KRCYRCKHVSFNDSL-----	555
CYLV	-----LVIGGR-----	-----LGLHATLGDTRCF-----	301
CNFV	-----HSANG-----VTFPGY-----	-----LGACVNSQLPKPTAV-----	396
MV-1	-----FVSVD-GV-----TVPLGGK-----	-----VGHYKFDGGYDEF-----	379
TV-1	-----FSLYS-GE-----PLAIRGK-----	-----VGLHHQHRSGKVFVK-----	357
ReV-1	-----FELVD-NE-----PLAIRGK-----	-----IGLHYRHLSSDFDKFK-----	355
BYV	-----EKKEYVVKRSKVVSSC-----	-----SVTKSPLEALAS-----	422
GLRaV-2	IVFGAFRCDI-----RYIEPADSGGV-----	-----QSSAKMKREEVRRVVKKCAAGAAAQSRKKIEEKYRDIQPDGGFPHL LAGNLNEVRRKVAAG-----	683
AV-1	-----DV-----GFTIESKYSMM-----	-----VSLQKTYV-----	441
AcV-1	RCKQAEER-NVGPADSTSPSAAESQAQSCSA-----	-----IGSSFRCGDSRKEYK-----	1053
BVA	-----GL-----CSRFSGRSFCPA-V-----	-----ISKAIPAGANVATII-----	554
PeVB	-----OKL TN-----	-----OKL TN-----	703
ArPV-1	-----RFTQRRF-----QLGPNK-----	-----RFTQRRF-----QLGPNK-----	256
CoV-1	-FGSL-P-----STHSFAVKEQA-----VKQPAQKPKQPSKPTSVNSTAQLVK-----PPLAKEQP--KVAQK-----	-----GWNVITRRKVV--TQPOQKQPEV-----	520
LCV	-----QSCSVK-----	-----HFVRSG-----	348
LIYV	-----SSVEVKL-----	-----QRYREG-----	287
GLRaV-1	-----DM-----	-----RVLWRRLL-----PV-----	279
GLRaV-4	-----NAGG-----	-----HYVGRVVVN-----EPI-----	374

FiVa	-----YLRR-----YEVGESFIKD-----	-----QF-----IDGPY-----	506
FiVB	YIRR-----YTPGAMMLYT-----	-----RF-----INGPY-----	493
RLMV	-----RNMNR-----FRIGREAVYS-----	-----RF-L-----HSSV-----	550
RLRaV	-----FIDT-----YQFPOSRLYS-----	-----HF-VN-----ARGDS-----	479
SCFaV	-----YLHN-----FALGDVRFN-----	-----HF-IS-----RNRV-----	508
CTV	QKASSPSTSSSSFNSTRSSDW--VNVGFSHRTTNKREPREYAGHRRIGN--FTFPRGTVVNTPVDERAYKRVLLRLDRTTACSFRLIRLLARLSGYPRLSDEF--FNKCVTSRF	-----	834
BcLRaV-1	-----YVNV-----YVAGGVFYD-----	-----KFRN-----	573
CYLV	-----YL-----TCYE-----	-----PEVDDF--IVSFVNGD-----	322
CNFV	-----YL-----SNVN-----	-----PLHNDF--FTCLTAGVR-----	417
MV-1	-----YL-----SFYS-----	-----PLRDDF--FSSVECGGV-----	400
TV-1	-----YL-----AFYS-----	-----PYSDDF--FTSHDCGV-----	378
ReV-1	-----YL-----SFYN-----	-----PFDDNF--FSSFECGGV-----	376
BYV	ILKNLPQSYNSERLKFYD-----	-----HF-----IGDDF-----	448
GLRaV-2	VLR-----FRVGGDMDFH-----R-----	-----SF-----TTHSGY-----	705
AV-1	YLKN-----YCVGGFKFIRT--IKGR-----	-----NF-----	462
AcV-1	LVDR-----	-----IL-----DF-----	1061
BVA	YGR-----KIYG-----	-----IRVNYRL-----	568
PeVB	GYDPGCGNLFPS-----	-----RRR-----LESLE-----	724
ArPV-1	-----YLLQT-----	-----KFTIGGRAT--EFFVR-----	275
CoV-1	KKVE-----Q-----QPVRD-----GVEL-----FKTKQGMFLFKT-----	-----FRSGGKIV--KF-VFRL-----	559
LCV	-----	-----Y-----EFFVTKF-----	356
LIYV	-----	-----EVFVSK-----	294
GLRaV-1	-----GV-----YVALP--H-----LLFRC-----	-----EDTGELF-----	299
GLRaV-4	-----WFYGRVAGSNKGM-----YLSL-----GDGKTSKCFLKS-----	-----FPTLREFLINDWAKG-----	419

FiVa	LINLHM-----GKGTVRF-----	-----EVK-----LYKKIFAWGDLCAP-RYTEHWRV--FGNASCVV-----	-----EREFANGFCYLTHIFHMSVM-----	575
FiVB	CINLHPS-----KAGRIGL-----	-----EVR-----CDRKFSPGCEICST--TYVNHNSV--FRDGRCLV-----	-----ERDFPNGLCYLKHIHFLCV-----	562
RLMV	EFLLRPA-----PGHCYVF-----	-----YVR-----VNTTWAGFKFTCS--SYSAALSQ--FTG-VLPPY-----	-----HSKMSPGYCYLDTLDRTAVK-----	617
RLRaV	EGVLVPL-----GGGWIKV-----	-----YVR-----IGTGWGYVFRKSH--ALSRVLSWY--VTGCAEFP-----	-----FDEGSVEGLCYLSHLNRVSLE-----	548
SCFaV	EVCLVGT-----TDKLVVR-----	-----FIR-----MGSRMTSFDEAL--EYAPYFLFF--KTGEVPEY-----	-----VDRFEAEGCYMNFLYYTSLT-----	577
CTV	VACIEPV-----ESGLVKV-----	-----HFR-----SDVFRASFPFDGQ--PIHPATA-----LTLLEVVSWD--WMTAFQNPQLKDGQCYIRHFAEVLSS-----	-----	907
BcLRaV-1	-----T-----DASSVT-----	-----YVRNLKAVTYWQSGDVSACATSYDAS--EYVNHFGELVLVHTNLSNRY--RCP-----	-----RSINGQCYLQVFVECCVG-----	648
CYLV	RYNIKVR-----GSGAVDI-----	-----IPMFSDE-----ITTTASRDY--LT--TYMRMSRY--IHDSILSR-----	-----HAPRGYCYLNIHFFLSLR-----	391
CNFV	REKFIIVRRVSGRSSVAL-----	-----IRR-CDK--H-VVSVVNELY--CR-VLRMRTTKT--IDYGLRM-----	-----KASEGFCYLNIHLWFICLT-----	489
MV-1	NYNFTPV-----GARRV-A-----	-----VVR-SDG--RVVARLPASRDF--AE--VYRMTTKS--FSGRLVSNF-----	-----HSPNGLCYLNIHWFICLI-----	469
TV-1	FYNVYPC-----GARQV-V-----	-----IKRLSDQ--KCVARLPCTREY--TL--MYEMHHRKN--FNGPMARRY-----	-----SAPAGLCYLNIHWFICLI-----	448
ReV-1	CYNALPY-----SNDRV-I-----	-----IRRVGDG--VVJARLPASRDY--LS--MYRMHLEKK--FAGPLARR-----	-----SASGFCYLNIHWFICLI-----	446
BYV	EIEVHPL-----RGGKLSV-----LLI-----	-----LPK--GE--AYCVVTAATPQYHA--ALTIARGDR--PRVGELQY-----	-----PRGEGCLYLAHAALCCAL-----	520
GLRaV-2	HLVWRR-----SSRSVCT-----ELY-----SPSKA-----	-----FLR-----YDFLPCSVDYAA--MFSFAAGGR--FPLVLMTRI-----	-----KYLNGFCYLNAHCRACAF-----	778
AV-1	LIRIDAS--KPRMASLSV-----	-----FVS-----GKIEYRCKFLCSKDYLL--AYKYYVGGSAFPVSWLFTY-----	-----SAPKLCYLNIHMYFLCVI-----	535
AcV-1	-----KQDESTLNI-----PLYEGFNVICVKNRPG-----	-----LVRILYKN--ILVKTVMANNRYMDITQVRSYGVCSK--SLKNLYRY-----	-----RDGEGYCYLNLMLRCCII-----	1146
BVA	-----VMDNVQF-----	-----L-----YRR-----AR--QLSGSVREA--RLGDILVNHGDRF--IHSDDF--SPIGGLCYRSMFWSADMT-----	-----	627
PeVB	GMYYQPA-----AENCCRICKDANCPSVFRRTSIPSEDVA-----	-----PVR-----QGVETPWRPVDVSTPNDQLQSK--LNKVGRIYL-----	-----NATHKKEKNGCYLNLFREMAF-----	819
ArPV-1	-----N-----AETPVIVKNQPG-----	-----TAR-----IFFNNTLINRQYFIP--NEALMSNPK-----	-----PYS-----SGKGLCWVN-----	328
CoV-1	-----S-----DESEYTLINDND-----	-----AAR-----KMYNLTIKNAFYIH--PECKVYNGR-----	-----PFA-----FYKDAFCWVK-----	612
LCV	-----S-----DGSEHRINNSRY-----	-----ATK-----EMYNLTFNNGFYIH--PMCTYPND-----	-----RFG-----SCKNFYCWIP-----	409
LIYV	-----A-----GKEDTRVLNDDN-----	-----AIR-----NLFNATLNGGKYLH--PEAKSATGK-----	-----RFK-----YKDGFCWLD-----	347
GLRaV-1	-----	-----	-----YGDKYWCWLQ-----LAVL-----	313
GLRaV-4	-----KSSSKHVT-----	-----FDPIK-----	-----NRNWRDRGRFWLP-----LY-----	449

F1vA	TGCRF-----DELHAKRR--LGRFPFTRSLKFLYLAKF-----FG-NNSLGTHTIIGWFT-----GKNTFHAHLKKGKLYD--VRRMPAHVRIGGEIDIRQSLQLISYREGS	665
F1vB	SGSRF-----DEKHATQR--LGRFPFTAARLRWYCSR-----FG-AHLSWPVHGTFT-----SRETFHV-----	614
RLMV	RGYLH-----NADHTVRH--LGRFPATKFRWFLQNF-----L--PIRPTRVLASVTV-----SRNNIVHIHTNGDG-----RRI-----	678
RLRaV	TGVPY-----RQDRVAI--LKDYPTATKLRWYKWW-----FG-KSALKVPL-----HCELNGKNVHA-----	599
SCFaV	VNRPF-----GVFTAMKT--LKGFPATKLLWFIRSR-----FG-GPGRKILVRGHFT-----SNKKIFHVDSSTSS-----RI-----	637
CTV	MGRIF-----FRRDVD--LGFPPYVFEVQHLERL-----YG-KAALRYGVGRQYS-----APRCFHCCYNDSP-----R-----	964
BcLRaV-1	CGIAF-----DARKAIEA--LRLPTLTKCLLAYVSKGLVPPSF-----L-----LRGYFT-----SRTLPHCDINST-----	703
CYLV	AGCAF-----RPAKNYFK--LGRNPSATDLSARISAY-----FG-FAAASYHIAGRYT-----GYNRFHCDNCSR-----	449
CNFV	GGLNF-----QGSFKTFKHLGRPRVFRVNLASF-----FS-SGATHIAVAGKFV-----SRGVFHVNDFFE-----	548
MV-1	SGTSF-----LRARKYFGR--LGAFFGVESFFSLLCNF-----FS-YHAVRIQIRGYFT-----STGIFHCDNVRG-----	527
TV-1	AGHSF-----NPARAYFSRGLGRFPRFSNFLGLVERY-----FS-YPATRVSIKGYFS-----RENLFHCDNFKG-----	507
ReV-1	SGHSF-----SSARGTFLK--LKGYPFRSDFIATVGKY-----FS-FPATRVGLMGYFS-----AASTFHCDNFKG-----	504
BYV	QKRTFREEDFF-----VGMYPKTFVFAKRLTEK-----LG-PSALKHPVRGRQV-----SRSLFHCDVASA-----	575
GLRaV-2	LLKGFDPKRFD-----IGAFPATAADLRRRMVSV-----LG-DRSLGLNLYGAYT-----SRGVFHCYDAD-----	833
AV-1	NNHVF-----DEKAHD--LGSLPSSGQLLKHIAVR-----F--PQSLNVKISGYFR-----RNGNFHCELHRG-----	589
AcV-1	FSKPM-----GYVRTAAE--LGSWPSFAVKCFIRKT-----FSKIPPVYVLS-----RGRYAHVGLLPR-----	1201
BVA	LGN-----RKMHKVVAE--LGAYPTRLGRVKELEKA--YKSDDF--PRKFFYFRVGRVLSA--SDAWSNDHCDFFTL-----	691
PeVB	-SKAFY--LSDKRIQIASE--LGPYPLCSAISEVLGDIG--FD-----SNPIIHINGDARAIYDGMGNRV-----QVV-----	881
ArPV-1	--AF-----AYFNKTIKSLPFVFKL-----YA-TQLIVAGLPAQFLKSCRMVERNLLHFDSKI-----	379
CoV-1	--AF-----ASQNKIPNNLQFPMPI-----RV-SVLISFGLSPVFLNNVITGKSLHDFMKV-----	663
LCV	--AF-----SKAKLRMPRLDYPYPL-----NY-GYLVQCGLKVMRNRRLRVKDDYHFHFDVNYNE-----	462
LIYV	--VF-----ADANRRIPEWVKPHCLL-----TG-SVLMSKGLWDFAKRKMVSVSHGLLHYDRKLE-----	399
GLRaV-1	NGNNLL-----AGSFESCISVRKL-----KRMLRFNVKLEKTD-----EANIFHVGNKPT-----	358
GLRaV-4	LNSELP-----LTQYPTGGLVRLFLTYDK-----FGPAPIVK-----SGKYYHYDVKGKK-----	494

F1vA	HELPAVGFNPRLRFVPEEAPVLENPKKILIMLQERSLVHALDYVVRVRYEPTKCFLRTRFLVSVFTIDLFAVPSEEVKIVVKKGDVYAWGDMMGENYAKHWRCVLNNE	780
F1vB	-----RIGG-----EH-----SMLTKNFV-----	622
RLMV	-----TSYGS-----	678
RLRaV	-----	604
SCFaV	-----	637
CTV	-----	964
BcLRaV-1	-----	703
CYLV	-----	449
CNFV	-----	548
MV-1	-----	527
TV-1	-----	507
ReV-1	-----	504
BYV	-----	575
GLRaV-2	-----	833
AV-1	-----	589
AcV-1	-----	1201
BVA	-----	691
PeVB	-----	881
ArPV-1	-----	379
CoV-1	-----	663
LCV	-----	462
LIYV	-----	399
GLRaV-1	-----	358
GLRaV-4	-----	494

F1vA	YEVEERNFRDGFYCLKHVYHLCAVEGLKDFEKHATQRLLRRYVSPAQFRRYVSIFFGDKLLAEYIK--GYFVRENWFHADLDGNLVDLRFM--KSRVRIGG--DL-----	879
F1vB	-----NLRD-----VK--QYF-----RIGG-----EH-----	637
RLMV	-----VDLFSLDR--SYRIGG--SDD--GAL-----	698
RLRaV	-----PRDISGFTY--TTRVGGSVV-QDA-----	625
SCFaV	-----YNLAKMGY--TVRVGG--DDD--EKSL-----	658
CTV	-----PMASFNG--YHKMGG--ED--NSL-----	982
BcLRaV-1	-----RVVSVNKF--GGSVVIIG--VTENSF-----	725
CYLV	-----KLYTLEY--LREAAVGA--EGED--EEVNT-----	473
CNFV	-----KFFSLRN--MGSSLIGG--DACE--KEQKK-----	571
MV-1	-----NLFNHRVQRRLRSARVGG--ENGEVPEMVMN-----	555
TV-1	-----RLHLSYNRINRAMIGG--DAADSSDNIAN-----	535
ReV-1	-----RVHWGSYRRLRFSRIGG--ETEGANEDLPN-----	532
BYV	-----FSSPFYSLPRF--IGG--VEEAP-----	595
GLRaV-2	-----YIKDLRRM--SAVIAG--KDG--VEEVVP-----	856
AV-1	-----RLWTLKAG--EEKIGD--DTD--ERAK-----	610
AcV-1	-----VSLENI--PNFLKGG-----	1215
BVA	-----DARDSSFDRY--FVGG--PKD-LPSSVSI-----	715
PeVB	-----GHFTA--SNFYFKLNLNDPDMALGGT--RGPSETNAETHEI-----	919
ArPV-1	-----IHNKWNLNNVVGA--SSEIDED--L-----	404
CoV-1	-----KNTKHINCHNYFLGA--ETTIPNAD--S-----	688
LCV	-----KPH--FLKFGSKIYVK--L--ENE--DGI-----	484
LIYV	-----VLSARAGVRD--FVGA--SNEAVQRED--	422
GLRaV-1	-----VSLAEV--DDRCFVGMAAKGGQSLVASVSN-----	387
GLRaV-4	-----HTK--FPMVVGVA--QNQVDTDDIT-----	516

F1vA	---VVDASKMKV--VNLAFDKVMT--KDSIFVKSVEKSMIDFHQDFEELQKSRPKTQVTVALNESQVALSKAYPEFQISFTHSSLSAHPVAAASRSLENELHWRARR--DYT	986
F1vB	---LTDVDMKMV--VNIASFKAEEA--KDSILTKSEKHVIDFHQDFEAIQKSKTKSVVNFLLTDSQVALSRAYPEFNISFTHSTLSAHPMAAASRALENDLHKWVKR--DYT	744
RLMV	---ALNDADRMKV--ISSVFATLSAN--RDSLTKSLEQDLITFKSEIHDLASSKQQRVPVFLNEADQTLINAYPEFKLVFTNSVHSDHAIAGRSLENALHKAFA-----	800
RLRaV	---CPPNDVEKMRI--ISDLMGKLNQ--RESILVKSIEKLDIFSKVSDLNKEKETVFPVPSVSEERVQVLLTKSYPEFNITFTHTSHSDHGAASRSLENALHXYAGS--NYS	733
SCFaV	---ITTSADLKA--LNLVYDKLNS--RDSILVKSIEKEMIDFSAVIESLNKQKEAIKVPFRMGESQVALTAAYPEFNIVFSVSHSDHDPAAAGRSLENALHXYAVI--NYS	765
CTV	---IITDTRLRA--VGSAYEKVKRN--TPDSSLVRSVEKDLIEFNQTLVDMHRSRGPVVPVQMSENQVMLTRAYPEFNINFSVSHSDHDPAAAGRSLENALVRKHAGT--DYS	1090
BcLRaV-1	---SLVQDQLQA--VSSAISRSQVN--RDSLTVRSVETAIIRVNEAARNERNKRPQVIPPYQMSSEKQALLVNAFPEFNKFTHTSLSNHALAASCRLENGLHKKAGS--EYV	833
CYLV	---FLDSYKEDQL--INQIVQTSRGS--KDSVLKNVEMDLSNHADAMRRIMREKPSLRVFPQLNETQAMVSRAYPNVDLIFTNTSPDPHMAAASRLLENITLSDFCEN--HYI	580
CNFV	---AITPLEKERL--INQIIESTRGH--KDSLILKMKEMVDLVEHVARLKRQLEKPERVPPHLEEQQSHIVRDYDPOYDILFTHTSHSDHMAAASRLLENFSLSDKCGD--DGS	662
MV-1	---VVTLEKEKL--ISQIIEIETARGH--KDSLILKLEVDLVDHITRLKRAQSKKERRVPPHLEEQQTLVLRDYPDYDILFTHTSHSDHMAAASRLLENLCLADKCGD--NFS	642
TV-1	---VVSPLERKEM--IAQLIDTARGH--KDSLILKLEVDLVDHISRLKRSQSKERRVPPHLEEQQTLVLRDYPDYDILFTHTSHSDHMAAASRLLENLCLADKCGD--NFS	639
ReV-1	---EITSSLKHKA--IESVYERVSTH--KDNLLARSVEKDLIDFKDEIKSLSKEKRSVTPVPMGEAVQSLTRAYPQFNLFSTHTSHSDHMAAASRLLENLCLADKCGD--NFS	702
BYV	---SDITPAMKQKT--IEAVYDRLYGG--TDSLILKLSIEKLDIFKNDVQSLKDDRPVTPVPMGEAVQSLTRAYPQFNLFSTHTSHSDHMAAASRLLENLCLADKCGD--NFS	964
GLRaV-2	---VLTDLQMHEN--LERAMRGNFGG--REALINAALDRDITIEYKNALKALNESKPAVVPVPMNETQSNITRNYPOYNLKFTHHTSHNAAAASRLLENITLTDACGS--GFS	717
AV-1	---HVESDMSMRMTEVNLNLAQVERAQLKDSALRAVESTLIEEHRIEERQMSQSSKPVVNVNLSNDSQQLALVKNFPEMLKFPVSVSHLHPMSSAVRMCFNALYSQKLGKRYI	1328
BVA	---NVLNSDEVVNC--HNRVSIQILKRTDPSKAFKAVEFDMINEYINVAQSKNRGDFIYGPYIEDEHQSMQMSFPFPHIRFVSHSVSHSDHMAAASRLLENITLTDACGS--GFS	826
PeVB	---DIILPQL--RATVIDQISKTSISECMYARELQOQLIERERARQFMQGLPKLTIPIHLESAERSKLSAFAPELLNIDFKPSKFSQHTMAACVRCMFCNELYASKFRDIDVY	1026
ArPV-1	---QCNYDFMQDL--VQKLLKTPK--ADNLTFTA--LNKAVEQLHWRTRQDTSVCLSTNQKIVAELEPPEFKISYLVGVSVSHLFTAVRELENYFCINFRFKGKSF	510
CoV-1	---HENYDVLDMN--LKKIFDKCSAK--SDNATLNNI--LRSRQSLKNCWDRTPNLSVCLSVQKQKFFSELFPFLKIDYLDKTFSSHALFTAVREASNYTYFKEMEFKNL	794
LCV	---TKNIEVLFQDI--SAGISGTQTR--SDNPLTTI--TSHLSNEIKQCNPKDVLVPTCMSSQKKELCCELPEINDFTESSVYTHALATAMRHAENYLSKKYGFKSFV	590
LIYV	---FRDLDLVEEF--AEARVELTANL--SDNRLDNI--LTRASDYKTKSKESKELDINVCMSDEKMITNLFPDQMSFNQKYSVNHGVFNAMRACENYFYSRKFNSDYI	528
GLRaV-1	---ALNQEDLFEFG--VSTANRNLVL--EGSTLVTHLDEKISELFMMKEDTLGKKNKCVTVALSAVAKESLTRAFFLITFDLQMSVSHLCAVAVRSCFNSLYASKYRGVVPV	496
GLRaV-4	WEDCNSDPLLRTA--VDSVLKRVTLK--ETSNTQINID--LFDKALHTLSSTRNEKLTISQHLTAEFELKGYGFLPYLGNAGNAPRNLKSLNAMRKNLKYAKTRFGVSVS	626

F1vA DIGGDLKNHV - VRGHTHVHCRPVVDPKDAQRRQRLEQYAFCTPT -----GVDDAKVFEAVKTLTACAQLAHKCDVQSKTLVSVQVDMNLQSLCEAMILKKKAKISYLVMT 1093
 F1vB DIGGCLMKHV - SKGHNVHVCRPVYDPKDAQRRQRLEQYAFCTPT -----NTDDEHMLEAVKTCSSCCSLVENCDCVQSKFIVAIOVQVDP LPLKLCQAMINKNSZIAYITMIT 851
 RLMV -----DSQRRVLRHHAYKRLKT -----D-SATPSSLSATSSLSACSNPIDVCTHKSVMYLVQVQVDP LPLVLCESMILRDTIEAYITMIT 880
 RLRaV DIGGCPYHV - NSRHSVHVCRLPMDAKDSQRRIMRHGYNMKL -----D-SDDVSNL TAVLSTLSFCSEIIECTHKSVMYLVQVQVDP LPLTLFEAWLRECDITVYATMIT 840
 SCFaV DIGGCPKHL - SAKHGVCVHCRPVLDAKDAQRRVVRHAYKSMIM -----D-TDKLEVSATSSELTTCARSITDCTHKSVMYLVQVQVDP LPLDLCTAMEKRCDCSITFATMIT 872
 CTV DVGGCPLFHL - RAGHSVHVCRPVYDPKDAQRRQRLEQYAFCTPT -----DQSDGKVGQVGTMTVNTSVCGNII LGCYHASEAMVMVQVYVDP LPLCTCRAMEKRCDCSITFATMIT 1198
 BcLRaV-1 DVGGCPKYHL - LAGHTGVHICRPVCDLKAQRKVLREHSIATETLP -----HNLVYKVTAVAGGCSLACSKMMS ECDVKTSCMVAOVYDLSLTDMANAMQMRGAAYVFFSLIT 941
 CVLV DVGGCPLHHYVFSKTRVHVCRPVYDPKDAQRRQRLEQYAFCTPT -----FVPSIHTSCAKVIDQCSYADYMMVQVYVDP LPLTCASMSKRRKVCVYVLTMIT 691
 CNFV DVGGCPKPHYEQPTTRVHVCRPVLDKDAQRRVLRNFELEKDSL -----KRNVDVGLTSLKNNL TSCSKVGVAGCHHKVRSMLVQVYVDP LPLVLCNAMVNEAKAVYVLTMIT 787
 MV-1 DIGGCPHHYRNSLKKVHVCRPILDSKDAQRRVLRNFELEKDSL -----HASKDVEENLYVNSLHTSCSYTISECRHTTPYMMVQVYVDP LPLSTTCQSMINKGADVYVLTMIT 771
 TV-1 DVGGCPLHYHNSKMRVHVCRPVLDKDAQRRVLRNFELEKDSL -----SNNQVPEDNVYVNSMHTSCSCLTISECTFETPSSMLVQVYVDP LPLRELCAMIKKSNVYVLTMIT 751
 ReV-1 DVGGCPLHYHNSKMRVHVCRPVLDKDAQRRVLRNFELEKDSL -----GSSKEPESNVYVNSLHSSCSLTVSECTHETPSSMMVQVYVDP LPLRELCAMIKKSNVYVLTMIT 748
 BYV DIGGCPFHII - KRGSYDHYHVCRIYDMKDAQRRVLRNFELEKDLVE -----NLREQVLEAQRVSVCPHTLGNVCNVSDVIMVQVYDASLNEIASAMVLEKSKVAVYVLTMIT 808
 GLRaV-2 DVGGCPLFHLNSKTRVHVCRPVLDKDAQRRVLRNFELEKDLVE -----GDDDKLIEGPRNVQVCHYPLGACDRESSAMVQVYVDP LPLRELCAMIKKSNVYVLTMIT 1070
 AV-1 DVGGSPYHQHNGREYEVHVCRPVYDFKDAQRRVLRNFELEKDLVE -----SLFSAEKQKLSANMSICGVGMGECTHPSKALMMVQVYDASTVEVAAMHAKGADVAYITMIT 824
 AcV-1 DIGGDLKYHV - MKGN-DVHICNPILDPKDGVRVYVNRVCEW -----NLAQVHDLNSMVGSKKVCCTYPAQNCVSCSTAVAEVYDITSMETASIMAKRSIDRVYVLTMIT 1432
 BVA DIGGDLKYHV - NNGHGDHVCPTLIDAKDASRAVIRKLSWKGEKP -----TLPVNLALASETKRTFCYKASLDCVSDVAVMVEVYDVP LPLKACISMSCRGISMLHALCA 932
 PeVb DVGGDLIYHS - MCKGHNVHICNPVDDKDAQRRVLRNFELEKDLVE -----ATPGTAVASTLSAPLRCCYSRAEVCADAMPATIAVEVYDITSMETASIMAKRSIDRVYVLTMIT 1131
 ArPV-1 DFGGNVLVSHY - RMGCDKTHICCPVIDIKDSARADIR -----TLQNLNLTVDHVGITLDCDLAQKCAQADRGMEVYDMSFVDAEAMISHGKORFFFYICA 607
 CoV-1 DIGGNLTHV - RAGTTPDVIHPCVDDKDAQRRVLRNFELEKDLVE -----ALSLDRKLGEFDSYDICTNKAQCHVSYDRAIAVEVYDMSLADAMADAMIKKDFLNSLL 891
 LCV DAGGDLTHYL - HKVTEDVHVCSPVLDKDAQRRHMQR -----SNKLDRLMGTCEKVDMECHLTOQCNVERPNIIIAVEVYDITSMETASIMAKRSIDRVYVLTMIT 687
 LTYV DAGGVDVSTL - RSGKNMNVHICNPVLDKDAQRRHMQR -----ATVIGLKGMEYETISFCNTKTEDCAVNRDIIIAVEVYDITSMETASIMAKRSIDRVYVLTMIT 625
 GLRaV-1 DIGGSVAHV - RNGDKDHCNCPVLDKDAQRRVLRNFELEKDLVE -----TVESVLKKEAANKNITYCQMDTRFCDHKAAPVGMVQVYDLDVFLAQALEKDKDKIFELCLMF 605
 GLRaV-4 DIGGNLSTAV - FSDCSNTHICMPILDAKDAQRRVLRNFELEKDLVE -----EGEFLAKRLQTLNNSISFCHDAPVKAVKSTIAVMVQVYDMLHKLKLIKAMEKKGALJARCCFMF 737

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F1vA PGEILDRLNFIPLLECEVAANPAMNSISYAFGSSV - YSHRLSAVVEYM - KRPFVWIGHNLFTEIEMFIRCDVNYKITSR - - - - EYCPQLSGVKILRYKRDASGITRILRPV 1202
 F1vB PGEILDRLNFIPLLECEVAANPAMNSISYAFGSSV - YTHQLSTITEYM - KTPYVVAENLFSIEMICVREVEVNYKIVRS - - - - QYCPRLSGVKILRYKRDASGITRILRPV 960
 RLMV PGEIVDKRALFVLPQLNCEVIEKPEDELLLYFSSST - - - - FSHLSVTLVLYM - NTPCVSGVGFSSVEMFARGCVNYVYVTKS - - - - DVCPKNSFTRRLRKRCDPDPVTRKIPRY 989
 RLRaV PGEILDGRTOFYVEDIECEIKINEGEDRLAYFPGSV - - - - YTHSLKTLVLYM - KNPLTVKGYLFSVEMTSLRSSVNLVYITKS - - - - DYPDTRQTLKRFRRKCDTDDVVRKIPRY 949
 SCFaV PGEILDGRSHFVSEVLELIEISSEDELIYVYFAGSC - - - - YSHSLKTVKLYM - TTPYLKGLVFLFCVEMNLSRNSVNHVYITKS - - - - EVSPLIRGPHLRRRFAHGHITRKKIPRY 981
 CTV PGEILDGRSHFVSEVLELIEISSEDELIYVYFAGSC - - - - YTHYTSIIECEM - RTPYLKGLVFLFCVEMNLSRNSVNHVYITKS - - - - SVCPRISETRKRLRFRKCDTDLRILKIPRY 1307
 BcLRaV-1 PGEFLTRDAFAHLNCAVDIIVSREDDRTVYFAGHT - - - - YSHLSMLLTFM - QTSFHLRGLVFLFCVEMNLSRNSVNHVYITKS - - - - SRCKPYEGSHLRFYFADGVTGKVIKIPRY 1050
 CVLV PGEILDREAREFHVLSDIITLREDDRTVYFAGSC - - - - YTHLSTLITQYM - TTPYVYENLFSIEMICVREVEVNYKIVRS - - - - EVSAPDQSHYLRFRKCDTDLRILKIPRY 897
 CNFV PGEILDREAREFHVLSDIITLREDDRTVYFAGSC - - - - YTHLSTLITQYM - TTPYVYENLFSIEMICVREVEVNYKIVRS - - - - DVSPTIDCSTKTRFRKCDTDLRILKIPRY 880
 MV-1 PGEILDREAREFHVLSDIITLREDDRTVYFAGSC - - - - YTHLSTLITQYM - TTPYVYENLFSIEMICVREVEVNYKIVRS - - - - DVSPTIDCSTKTRFRKCDTDLRILKIPRY 880
 TV-1 PGEILDKRECFHDDLGCIDIIIDHEDSITYKFGSSC - - - - YTHDLSVILVYM - TTPVLLVNNLFSIEMICVREVEVNYKIVRS - - - - DVCPSMDCGKTRFRKCDTDLRILKIPRY 860
 ReV-1 PGEILDKRECFHDDLGCIDIIIDHEDSITYKFGSSC - - - - YTHDLSVILVYM - TTPVLLVNNLFSIEMICVREVEVNYKIVRS - - - - DVCPSMDCGKTRFRKCDTDLRILKIPRY 860
 BYV PGEILDKRECFHDDLGCIDIIIDHEDSITYKFGSSC - - - - YTHDLSVILVYM - TTPVLLVNNLFSIEMICVREVEVNYKIVRS - - - - DVCPSMDCGKTRFRKCDTDLRILKIPRY 860
 GLRaV-2 PGEFLDGRGCVYMESLDCIEVDVHADVYVYKFGSSC - - - - YCHKLNIKSIDM - LTPAFVTLGNLFSIEMICVREVEVNYKIVRS - - - - AVSPEIRGVTILRYRRAKCDTDLRILKIPRY 917
 AV-1 PGEFLDGRGCVYMESLDCIEVDVHADVYVYKFGSSC - - - - YCHKLNIKSIDM - LTPAFVTLGNLFSIEMICVREVEVNYKIVRS - - - - AVSPEIRGVTILRYRRAKCDTDLRILKIPRY 917
 AcV-1 PGEFLDGRGCVYMESLDCIEVDVHADVYVYKFGSSC - - - - YCHKLNIKSIDM - LTPAFVTLGNLFSIEMICVREVEVNYKIVRS - - - - AVSPEIRGVTILRYRRAKCDTDLRILKIPRY 917
 BVA PGEFLDGRGCVYMESLDCIEVDVHADVYVYKFGSSC - - - - YCHKLNIKSIDM - LTPAFVTLGNLFSIEMICVREVEVNYKIVRS - - - - AVSPEIRGVTILRYRRAKCDTDLRILKIPRY 917
 PeVb PGEILDREAREFHVLSDIITLREDDRTVYFAGSC - - - - YTHLSTLITQYM - TTPYVYENLFSIEMICVREVEVNYKIVRS - - - - DVSPTIDCSTKTRFRKCDTDLRILKIPRY 880
 ArPV-1 PGEILDREAREFHVLSDIITLREDDRTVYFAGSC - - - - YTHLSTLITQYM - TTPYVYENLFSIEMICVREVEVNYKIVRS - - - - DVSPTIDCSTKTRFRKCDTDLRILKIPRY 880
 CoV-1 PGEILDREAREFHVLSDIITLREDDRTVYFAGSC - - - - YTHLSTLITQYM - TTPYVYENLFSIEMICVREVEVNYKIVRS - - - - DVSPTIDCSTKTRFRKCDTDLRILKIPRY 880
 LCV PGEILDREAREFHVLSDIITLREDDRTVYFAGSC - - - - YTHLSTLITQYM - TTPYVYENLFSIEMICVREVEVNYKIVRS - - - - DVSPTIDCSTKTRFRKCDTDLRILKIPRY 880
 LTYV PGEILDREAREFHVLSDIITLREDDRTVYFAGSC - - - - YTHLSTLITQYM - TTPYVYENLFSIEMICVREVEVNYKIVRS - - - - DVSPTIDCSTKTRFRKCDTDLRILKIPRY 880
 GLRaV-1 PGEILDREAREFHVLSDIITLREDDRTVYFAGSC - - - - YTHLSTLITQYM - TTPYVYENLFSIEMICVREVEVNYKIVRS - - - - DVSPTIDCSTKTRFRKCDTDLRILKIPRY 880
 GLRaV-4 PGEILDREAREFHVLSDIITLREDDRTVYFAGSC - - - - YTHLSTLITQYM - TTPYVYENLFSIEMICVREVEVNYKIVRS - - - - DVSPTIDCSTKTRFRKCDTDLRILKIPRY 880

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F1vA DAKLKTCC - SHKCNVYLYTELFKFSQVYEVYVNTCTQINSKTEFEAWMNVYKCSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 1315
 F1vB DAKLKTCC - SHKCNVYLYTELFKFSQVYEVYVNTCTQINSKTEFEAWMNVYKCSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 1073
 RLMV NVKTKTCC - PGCDYLVLDKSKVFSVFEHVNVTCTVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 1102
 RLRaV CAKTRVC - KPGCHKYLYLDSKFMVRLDHTMNTCTVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 1062
 SCFaV CSKTRVC - PGCDYLVLDKSKVFSVFEHVNVTCTVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 1094
 CTV DQGRSACC - LPGAQYLYLDADFEVYKIEYVYVNCVNVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 1419
 BcLRaV-1 DQGRSACC - LPGAQYLYLDADFEVYKIEYVYVNCVNVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 1163
 CVLV CKKTRKC - LPGAQYLYLDADFEVYKIEYVYVNCVNVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 913
 CNFV CKKTRKC - LPGAQYLYLDADFEVYKIEYVYVNCVNVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 913
 MV-1 CKKTRKC - LPGAQYLYLDADFEVYKIEYVYVNCVNVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 913
 TV-1 CKKTRKC - LPGAQYLYLDADFEVYKIEYVYVNCVNVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 913
 ReV-1 CKKTRKC - LPGAQYLYLDADFEVYKIEYVYVNCVNVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 913
 BYV DKLTKFC - LSGDYIYLVLDKSKVFSVFEHVNVTCTVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 1030
 GLRaV-2 DKLTKFC - LSGDYIYLVLDKSKVFSVFEHVNVTCTVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 1030
 AV-1 DKLTKFC - LSGDYIYLVLDKSKVFSVFEHVNVTCTVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 1030
 AcV-1 DKLTKFC - LSGDYIYLVLDKSKVFSVFEHVNVTCTVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 1030
 BVA DKLTKFC - LSGDYIYLVLDKSKVFSVFEHVNVTCTVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 1030
 PeVb DKLTKFC - LSGDYIYLVLDKSKVFSVFEHVNVTCTVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 1030
 ArPV-1 DKLTKFC - LSGDYIYLVLDKSKVFSVFEHVNVTCTVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 1030
 CoV-1 DKLTKFC - LSGDYIYLVLDKSKVFSVFEHVNVTCTVNAKTEFEWHTYTKSSKSRVTSKGVVHRDVTIPLHEMAFVAVMLAAGVKARMSAEYFSKLL - AVISGDATYQMIKYA 1110
 LCV NKLKTE - - - - HMKIKMKACAFHNLVEYANVTLRLEDEKAFYVLSQYRKAISISIRGGKVTQVQADMPKAVAGLIGAVAGVRLRLEQSHKAARVA - YLEYQYAPTLKRCVLQ 906
 LTYV DSGFVMT - - - - HIYIKEDREVFSSMIEYVANTGKIDDKMVEVYTSQYRAKTVTIKGVKVTQKTRIRKELIPGFIATIMSEGIARERHTHYLAKML - YTSYHGPSVNTIFRL 844
 GLRaV-1 ADG - - - - FLSFRQYVLDSDVDRVYVYLLNTSFAFVDRTEYAVSARSQSKTHVIGTRVQVADMPKAVAGLIGAVAGVRLRLEQSHKAARVA - YLEYQYAPTLKRCVLQ 821
 GLRaV-4 LDGGSVSNL - - - - KLVDRDFVRVRLYSANVCNTLDDRTYVYVLSDRSQTMMIYVGSKLVHKNVDSINDVIVELPGTFLKAVKRRRRAVEQAKS - - - - NPGFRKLLAN 950

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F1vA VTEKLSKTLSSLNHKITEYLKAILSADFVQFLTQERAFE - - - - DVTEYAEVQV - AYDLKP - - - - FGSVPD - - - - -NEELNVLVENIE - - - - 1389
 F1vB ISEKMSLAVNTRVYATLKAILSDFDQFLTDERCFE - - - - EVSEYAEHNA - SYQLEQ - - - - FGSVKD - - - - -NEEMNTIVNSIT - - - - 1147
 RLMV IGEKFRSVMQDFDKYLATKIKMLKDAFSLFELVDDEPLD - - - - TIGEYAEVLD - DVKLSA - - - - VGSJPE - - - - -HEEEDKTIIVAAVK - - - - 1176
 RLRaV LKERFLAVMSSMREYVAKVMKSFKEYFLFEMDIEEPT - - - - TISEYAEYSC - EVDVNR - - - - KGF LVE - - - - -DEEIKLISSSQV - - - - 1136
 SCFaV LEEKFKGALFNAYVTSVKNMLTDGFGFMEIEDPFE - - - - EVGEYHDLV - NVDISP - - - - SGE LVE - - - - -SEETSLEAEVK - - - - 1168
 CTV ISEKCRDLFLGQDAVERCVKSYLNSFNMSFVLDSDPLL - - - - TISEYSELVD - PIDLPG - - - - FGG IVO - - - - -GNETRLMEDGVSAL - - - - 1496
 BcLRaV-1 VSEKLRHMFRLFRSKFTTAKRICKDAFDFTLEATDIT - - - - SIGHTIEIVV - NVSLQR - - - - SGS IAP - - - - -NEEFTNIAQAARLI - - - - 1240
 CVLV LKEKYRGLKQSFNDYLLTKGFFADVLLMEFLDLDADPT - - - - YDNFSEITV - GIKQOG - - - - FGA IDO - - - - -GEVQALLNSRC - - - - 986
 CNFV LKELLARAKRSVREYEMKTLKGFSDVLLLEFLDLDSDS - - - - DMEEYSEIRV - RVETNK - - - - FGE LIT - - - - -NEEQVILVANKV - - - - 1083
 MV-1 ISEKTKDLKRLNRTICDSFRKLFADALLMEFLDLDSDS - - - - YLDAFSETV - HISLRG - - - - FGSVPS - - - - -NEPEIMTADKS - - - - 1066
 TV-1 LNEKLDKVRQFNKFCVDSFRKMFADALLMEFLDLDSDS - - - - YLDSFSEYSV - RIRVAG - - - - FGA IVP - - - - -NEPEIMTADKS - - - - 1046
 ReV-1 ISEKTKDLKRLNRTICDSFRKLFADALLMEFLDLDSDS - - - - YLDSFSEYSV - RIRVAG - - - - FGA IVP - - - - -NEPEIMTADKS - - - - 1046
 BYV ISEKTKDLKRLNRTICDSFRKLFADALLMEFLDLDSDS - - - - YLDSFSEYSV - RIRVAG - - - - FGA IVP - - - - -NEPEIMTADKS - - - - 1046
 GLRaV-2 IREKLRNMTLNFNERLLQLKRVAFATLDVSLDLDSTLE - - - - SITDFAECKV - AVELDE - - - - LGCLRA - - - - -EAENEKTRNLAG - - - - 1366
 AV-1 IANIKQIRELSSAYFTNMLKLNLSNMDFSEIDVNTGLE - - - - TVTEYVELEV - KVKVAG - - - - FGSFDE - - - - -SGSETEVLRNLI - - - - 1118
 AcV-1 IHESTLVKAAAYDVVKLSSSFPFLGDLQSKSIDDFPT - - - - VLGESITITR - AAKFPC - - - - SGGVNV - - - - -GETRYI - - - - D - NMVNTLLEAEVA - - - - 1736
 BVA LKDKFKDSKLRVLFKFKLHKLKFLDVFCDMLDEIYK - - - - VCDQYTVLRTIDSTAPP - - - - SSSLNV - - - - -DME TAEIESYVDRAV - - - - 1232
 PeVb IKETVTSVGRSCEAVIKFLFELFLPVKGLVLELDLKYR - - - - PIANFYDVEV - HDVPIITGNMDESAGETAAAIKFEFY - - - - RNQKRFVVKTYREIEGVN - - - - 1449
 ArPV-1 LKSVFSKFSQACYKIIALLRLLVLMVGMVDEADNKGKFF - - - - DNFSNVINE - QVITNK - - - - -DEQSSITVOQAEALGRGKFEV - - - - AH 907
 CoV-1 LSKLFFKVNKYCYQVLETMRYLFGDWMVEAYSSQGSQYR - - - - YVSEIECVQV - TIEILT - - - - SGT FVD - - - - -ILDTTFERSVKDC - - - - -GMADILKDNFPEMKDD - - - - 1203
 LCV IAYVLLKFSNTHDFLMDVLYLTPKLSLSEVTSNCSQVIRE - - - - FIGEY - RFQV - YHITZIG - - - - -SKRSILTESEFKF - - - - -KFS 982
 LTYV IMHFLGGTKRFYVESLVDCLKFLTNSDYDITVNTSRIE - - - - DLDKWVFVEQ - NVTIT - - - - -DA - EDQPSILIQSVKTLFSKYSEDVYERGD - - - - 929
 GLRaV-1 VNRKLSGFSGMNEYALTMLQALGSLNDVLL - - - - MDQNFVRVTVPATVTLHL - VAETNP - - - - -FTD - FDSMILLDEGLMAYR - - - - -LHL 896
 GLRaV-4 I - - - - FSPRRILSIFVSAIRRLKPSKIRKTF - - - - DQLLDDPGLISDCADVTV - - - - -TETSNDVSD - - - - -VLLNKILEVDLNAVK - - - - 1021

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F1vA	FSVVGYQHSLGACESNLEWHFREMVAAYTANLV-IPTGY-GNVERLIVMSCAIPSVRVL-LCSFMDEED-GTY-----VGYVNHALSVPNIYSH-----	1724
F1vB	MGCVSHQLNHIGGESTLLEWHFKQMVAYITASVV-LPSTA-TKIEKVITVSCAIPAIVRLL-LCSFLPEDDGGTY-----VGYVNHGLSVNPVVSF-----	1481
RLMv	EYCANLFAITHFQKPELYSVEFFRRGVAASLAAVS-TRGVK-LDTMGLVTLSTVMPMLLRVK-LAFPF-VNY-SPH-----AAVYLVAASDFPVVSY-----	1489
RLRaV	EYNIASYTHDRVGPPELTKSEFFRRCCAAALAAVS-TRGVK-FDCVGVQLSTVLMTRKL-LACVL-VTD-NAH-----INVYRHAGDDPFIFTY-----	1443
SCFaV	EYANCFALCEFGAPLEYAQEFFRRGVSNFLACIS-TRGVI-LDVTGVVQLSTVAPMIVRRI-LGLVF-SET-SPH-----LAYIKHAASDFPIQAY-----	1488
CTV	EVGSNFLFKKVFQKPELTGEDTFRRTVSMVLRPKA-FDKLS-VDAKGLRCSGVIPGLVRII-LSSLF-SED-DAW-----VGYSKHVESLPIVTF-----	1835
BcLRaV-1	DCTLSIAHNE---KPTSLTLDQMRCLLTDYISKAC-VFGVSPISLDGILTLGVLVTVFRVK-VSRCL-DENTSTY-----AGYVNNNAIDSPLIAYLRR-----	1482
CYLV	ELNLLNLAIRIIGPSDTLKKDMFNRTVSLVSSAF-LDRFT-FSPETFIRLSTVPMVVRKL-LVSFF-SDDFSYV-----VGQVYGVDDFSAFYARR-----	1315
CNFV	EINLNAFIAHYVGGQPKERIFHQNVVRYSLHLC-HDGF5-LDLFALLKANVVSVLRSF-LAEFF-NEEYDSY-----FGRVKFVGVKFGFEG-----	1399
MV-1	EFSNLALLSCKLGPADTIKKDLFIRSVSVSDGV-LDGYD-MSVM5YVKLSALVPLMARKF-IVSFF-SDECPY-----VPLMR5AASDFSAVEYLALVFNK-----	1388
TV-1	EHSNLALJACKIGVADTLKDMFIRTVSLVADGV-LDGYD-LTFLSFVKLTALIPMFVRKL-IVAFF-DDECCY-----VAIVKHGVRDFSAAEYLRIYFN-----	1368
ReV-1	EHSNLSLISLIGVADTLKDMFIRTVSLVADGV-LDGYD-MTLFSFVKLTALIPMFVRKL-IVSFF-DDDLCEY-----VGIVKHGVSDSLAAEYIARLNV-----	1365
BYV	KISIEVLLKQISPADSTASSALYRVLSEILSNFR-TMGEH-GIFTKVLFLCGFLPVFVRCK-VALCV-PGDMATY-----ARFLEYGVDDLFLFLGR-----	1414
GLRaV-2	EVVVRNVVTVHGLSTTATDGVIRGVFSQIMSHLL-VGSTG-NVAYQIAIAGVVPVLLKVK-VSLIF-IMREDTY-----SGFIKHGISEFSLSS-----	1688
AV-1	ELVALIHRVDE---NSTGTEELYRCCASIFSNLC-HRNGG-GL-YDVLCLSGVPMVSRKI-LSLIRGEKNISLY-----TGFLSYASDFLVLLEQ-----	1507
AcV-1	TDKDN---LSADILFEALKGAYFSVPLTRNKWLNRLSVLENVGYKSLVRRKI-IAVVF-EESTAAS-----VIRRIIRKTCDFLKEELV-----	1970
BVA	GSNLFNFRFRASDDFNADITDFF-LVTDALILWP-S5GVV-SVAYGVTALGPMRMMVRKA-LLPVV-GADSGFHGLMVCSDSPDCNIVRLIHFVKYVVSALTEFAC-----	1511
PeVb	DEFVN---VIRRIIRKTCDFLKEELV---KFACTIDIKDPKIGRITRLV-----DADLSEKSVSTRDVVY-----	1768
ArPV-1	-----TFQTF5KVSQEMDEIDEMD-----SIDLAIEFG-----KWLVLNHHDFEFKSLSFDEQ-----	1090
CoV-1	SRGFTLKNLTKQCRDYLDITIMRVGLKVM5RFDPISELD-----ECVNIIDDDKVN5-----NEKTTVINNMDDFDDITH-----	1381
LCV	-----VLKIP-----LSSCCVSNLQRAA-----	1107
LTYV	-----MTCVDSVNYLKR5-LEKIL-----	1052
GLRaV-1	-----SLKVVARAEFKDRVSGVVEEMGYIGD5LNVQVTCCLTAAAYLSS5YEK5AILL1L-APKFRFY-----IGSVGYGIAALRCKGGEY-----	1224
GLRaV-4	-----KIKRPIF-----ICSITLGAVMKNLARLS-FLMMP-VEDCREV-----C-----IGMFSNINLCAYNTVREPT-----	1350

F1vA	-----LAYKARHFGLSIKEYIRRCVS-----DV5SRVGSLLNSVSDASG-----ITA	1767
F1vB	-----LTLKAKQYGLSVKAYIRDVD-----KVC6GVEALVTSVKDATG-----VTH	1524
RLMv	-----LSCAVASGLVLD5VSVLVTASINEAFD-----GIVT5KMKGCKTALKECTVS-----RVVARF-----C-----NGLTTP-----FSA	1553
RLRaV	-----LSDLF5SVRHLPNELCTYCAQVQDYINH-----LGLSDR5DL5M5YIASKCVK-----RIFSTF-----C-----KAQVTPAGQSTVELVTS	1517
SCFaV	-----LKLCDVSHVFTRESLELYVTDLCKSLVS-----SVLSKDVLLGVKTLIKDNMVT-----RVFSRHLRPSYIPIKVECAVSSALSS-----LKA	1565
CTV	-----VKRLSYSLERCKEACVAFIVDSAKKILK-----SLTSEFNESIQNSDLTSGAKSL-----VGHVSS-----ILY	1894
BcLRaV-1	-----ECLRLGVGIGEYKCLIRDTISEM5A-----QNMKEYKQCCSDISGKVKEGTE-----W-----	1533
CYLV	-----NASDAYHSILN5L5CR5SE5YLD-----KVIDK5FETVTKSTLETLP-----	1359
CNFV	-----IVALK5E5A5D5DA5KA5IGDR5FE5FV-----N5L5R5CA5AH5TEK5F5E5ED-----VNK	1449
MV-1	EVQGHVELIRDSVTDCLRAVGGKAAARTEAVLDLVEQRLELISR-----RMVK5IDEVTKR5LDVAA-----CKR	1454
TV-1	NLQGHVHLKCKEVLQSP5LPTLQ5R5G5E5V5A5QR5L5E5G5MT5L5K5-----QV5A5E5AS5EM5N5L5C5N5RI-----VKC	1434
ReV-1	NVQGHFMHCKEYIDL5T5IR5ERT5DES5L5HL5LAR5DEY5ISER5-----AAV5K5LD5GL5R5GR5VD5NT5-----FKT	1431
BYV	-----SVNSIKNLCVVAAGLVD5IVDSVVLK5L5GVAK-----ERVL5FK5K5I5K5N5L5N5V5FR5K5AKV-----VTR	1473
GLRaV-2	-----VTLFKGLVDELK5V5Q5GV5F5EK5MH5FK-----EATQ5AIR5TV5Q5V5P5VA5VD5ALK-----CA-----AGR	1745
AV-1	-----TLRKA5TR5FH5NAV5DL5L5E5K5F5S5IM5TV-----INR5YM5KG5F5AV5G5S5EL5K-----RA-----CSA	1557
AcV-1	-----V5ML5VR5PE5NV5AV5EN5LV5KA5YD5H5AY5-----QIY5T5Y5L5AL5SA5V5H5SA5KA5A5AV5NT5IGD5-----AGG5V5S5-----L5T5S5VAK	2040
BVA	-----SQVDA5AML5FR5TS5AG5VADA5QA5AA5L5CAM5NQ5VDD5IL5NSMR-----TCR5DR5ALE5IP5KN5AS5T5L5CN5L5SD5VCA-----SA-----M5ERV5R5	1586
PeVb	-----SS1GN5K5SS5CG5K5IK5SF5FK5TPD5-----	1794
ArPV-1	-----SML5T5FK5L5ISE-----	1107
CoV-1	-----ILND5IDEL5MT5SG5GR5NR5TK5V5L5QI5ET5L5K5FR5D5CL5K5L5TK5FA5-KALAKY5--VYL-----C-----VKA	1437
LCV	-----RTMYN5L5TKR-----RNSDWE-----DQLSK	1127
LTYV	-----SYFS-----	1056
GLRaV-1	-----GRASK5LM5GVA5L5AL5L5TAK5KGAS5RAAS5LQI5--VFPK5--SDF-----R5GD5Y5EG-----V5T5	1267
GLRaV-4	-----VLN5K5VE5L5SNF5--LL5L5QR5NM5GM55S5V5F5AL5QR5V5V5DE5PT5KV5D5V5AD5V5DK5--SHF5--EI5--NSD5VEEV5--INN	1412

F1vA	VSNAWDFKTKAKEF-----LPKMLISK--LPFF-----SEAR-----NFG--KNDKAAD5E5I-----	1811
F1vB	ISHAV5YK6K-----LWNA-----LPNF-----IAAS-----HDD--SKDEDVNEE-----	1559
RLMv	TSAKFRDLASGVPSFN-----VTSIR-----K5VRDR-----TARHFARIL5Q5P5-AIS-----DEAPL-ELVDFP-----	1606
RLRaV	AESCIESL5G5AVP-----LDEIA-----K5IAED5-----VGD5L5SPV5-Q5P5-VNG-----E5ATS5-E-----	1561
SCFaV	TEEK5VAK5SG5Y5FA-----ADNISA-QYLK5VANNR5GF5KH5K5FSNT5AVV5VA5E5DD5CH5TAP5E5I5Q5RM5H5G5--S-----D5E5L5S5-E5IST5F5PE-----	1642
CTV	TSSGVINKAG5AV-----ATVKAVG5D-----ISGRVK5RMR5PR5-SL5R5-----HF-----DEQ5TS5-E-----	1940
BcLRaV-1	-----HARYQS-----L5K5R5L5TRARR5-Q5TS-----SDD5E5-D-----	1397
CYLV	MYSSLL5L5K5GVV-----ESLYAK-----L5R5K5L5SDL5FR5GD5NG5-----DD5GD5-E-----	1489
CNFV	VTACYTRKQ5RA-----IATS5NR-----AS5R5F5VR5M5NR5-RCS-----DP5GT5-V-----	1492
MV-1	ISS5CS5IS5GAV-----TKMYKA-----AR5K5R5CD5-----D5EAS5-D-----	1465
TV-1	ASNSYGA5VTG5L-----KKVYGF-----SKHF5SAL-----D5G5D5-V-----	1462
ReV-1	TANSYR5K5V5RVV-----	1484
BYV	TSS5-----	1484
GLRaV-2	VYNSFAS5RRT5FG5K5DNG-----SSS-----EDACE5-E-----	1770
AV-1	VNNV5P5M5L5K5P5-----QEG-----DD5GD5-V-----	1578
AcV-1	VLDWF5NQ5RQ5N5PP5GLG-----P5T5P5A5E5M5V5L5H5I5-----NEDL5-L5DD-----	2063
BVA	VSNV5ASNS5FQ5SD5IE-----DVNF5D5DAL5TL5Y5MS-----ELE-----L5EG5GL5E5AV5EQ5-----	1855
PeVb	YF5S5IDEG5T5G5EV5DVN-----NECADNP5ESTV5QEDA-----DRK5SVNI5D5SNHP-----	1135
ArPV-1	AQDD5ED5F5E5D5PLD-----R5L5DL5KNV5IN5VE5DL-----R5F5SL5K-----D5DS5DES5-----	1478
CoV-1	AVASL5T5FL5K5SP5D5-----	1149
LCV	MLDD5TK5L5G5ST5LR-----	1063
LTYV	-----HERAD5E-----	1063
GLRaV-1	FYRQ5RAER5K5GAA5IEPS-----RR5EG5E5AM5DD5L5DE-----ATC5GT5S5E5VE5QE5K5ED5L5T5K5T5-ED5-----T5D5AD5DES5V5ESSQ5-----	1333
GLRaV-4	FR5N5IK5DL5K5NAK5L5E5K5R5PV5K5F5E5G5SS5G5K5K5A5E5TAK5P5-----VAT5AD5K5RR5K5ESS5K5R5-ST5GD5CG5IV5IN5DE5H5I5E5TR5--AEAT5L5KE5K5E5K5A5E5PV5K5V5K5AC5N	1504

F1vA	-----FYDA-SDV-----P--GLKGGNRL-----LLTTARRWCLAL--	1840
F1vB	-----FYD5T5SSC-----E--GLK5G5K5T5FA-----NYV5VK5IR5Y5L5F5S5-----	1591
RLMv	-----ATEE5ILED5L5FESAP5SF5G5ED5DRV5-----LL5R5-IR5-SF5-PFF5SR5G5SK5P5-----GL5FAG5K5SRV5-----LEFL5YHF5ST5L5RE5I5PL5-SLQ5L5WY5FL5V5GR5K5V5F5SDC5-----	1698
RLRaV	-----S-----LL5K5R5L5R5-RFV5V5G5F5-SLY5TR5P5-----GL5G5G5R5CS5NA5-----IV5R5FL5NY5IS5GL5VQ5R5-----V5FA5-----	1612
SCFaV	-----G5CEEE5V5H5DFI5-----ED5G5L5S-----LL5NS5-FK5-SYLL5Q5V5Y5TER5K5TP5-----GL5G5G5R5RR5G5VM5ML5MR5LY5N5FL5DCV5S5IDIR5GV5Q5S5L5Y5L5AV5K5DV5--IFTN5-----	1729
CTV	-----Y5S5AS5DC5-----EL5D5-----SL5F5E5TP5-----GL5R5GNAR5-----	1967
BcLRaV-1	-----FFDATEED5-----LDS5-----G5E5TS5V5K5G5-----GL5G5G5R5CK5S5I5S5-----V5TL5FF5GLK5-----	1589
CYLV	-----FF5T5S5ED5-----EL5L5E5K5P5-----GL5F5G5NG5P5-----	1420
CNFV	-----FH--DS-----I5S5F5E5P5-----GL5R5G5S5AE5-----	1507
MV-1	-----Y5S5AAS5D5ND5-----E5TS5AK5G5-----GL5AG5GN5CR5-----	1518
TV-1	-----Y5S5AD5G5G5-----EA5E5T5G5-----KL5R5G5GAR5KE5-----	1488
ReV-1	-----Y5S5AD5SDC5-----E5S5Y5R5G5-----GL5R5G5G5I5P5S5-----	1485
BYV	-----Y5F5S5C5DE5K5-----P5-----GL5R5G5G5S5R5FT5L5R5-----LLD5IFFN5--	1513
GLRaV-2	-----Y5F5S5C5DE5G5-----G5-----P5-----GL5K5G5G5S5V5G5-----F5-----	1790
AV-1	-----Y5F5D5A5EN5-----P5-----P5-----PER5G5GL5K5G5S5PRN5-----Y5IV5H5V5S5L5IS5NFV5-----	1612
AcV-1	-----FF5M5V5D5V5-----E5S5IDDL5-----L5SETP5-----GL5R5G5G5V5L5NR5NL5-----	2095
BVA	-----Y5K5S5AC5DG5-----S5DTP5-----GL5G5GN5L5AV5H5AS5F5-----LAS5L5F5SV5G5-----	1674
PeVb	-----AE5LET5V5RR5FI5-----DE5Y5Q5AF5D5V5-----AL5DL5KE5EGY5--G5E5L5E5L5D5K5P5-----GL5M5G5GN5-----	1902
ArPV-1	-----TS5IF5V5IR5T5N5-Q5LYN5K5F5L5A5E5DM5-----E5I5Q5S5-----TV5E5S5-----GG5HK5R5T5N5FR5--K5CLQ5-----I5N5AD5I5Y5L5T5NS5IV5F5F5G5N5K5-----	1202
CoV-1	-----S5T5D5D5E5S5Q5S5-----E5G5IL5TR5HER5--LC5IF5L5ATE5K5LEP5-----S5G5R5L5R5ML5R5--K5FL5I5-----AR5K5L5P5NC5F5-----	1533
LCV	-----K5Y5E5H5I5E5TM5-----S5LD5QL5D5F5-----I5G5N5E5G5S5G5L5G5S5F5I5-----Y5NH5NN5L5VR5K5V5NQ5Y5Y5G5TK5-----	1197
LTYV	-----Y5IF5P5G5Y5D5S5-----F5-----S5E5E5S5-----G5DY5G5D5E5N5T5L5D5SR5-----	1090
GLRaV-1	-----HTA5Q5SH5F5-----T5TS5V5N5E5SK5HE5--S5G5IL5AD5-----G5K5V5E5R5K5E5E5P5-----	1368
GLRaV-4	-----TEEP5AAQ5TEP5TRI5PT5-----P5SY5I5E5L5DE5RNA5IF5E5EN5LEAT5VD5-----D5VL5SD5AE5--G5K5T5G5D5TR5M5K5A5-----	1561

F1vA	-----NSLLKGVKTK-----VNMW-KVE-----NEKRSLYNEVMRE-----LNYIVDEGK-TSSFA-----LTKFMNIFQN	1894
F1vB	-----SKFQETKNN-----VNIW-FLE-----RERLRLRNEVLRE-----INYLTTNGS-FSSYE-----LTKFVNNFQV	1644
RLMv	-----GGLMSIILCCINSGGDSVLLCSLPD-----VSCV-FSDSPN-----LRGGLRGGNAGD-----FWFRYSVLQ-DFAL-----RYIFNSHTL	1767
RLRaV	-----DLVTKALESVRAFISSVA-----P-----RAL-LSL-----GALS--VSVS-----VGFVFPNLV-PVPL-----FLNLFSGHL	1668
SCFaV	-----LPKYCLAVLSYNIPLMKCSFP-----VL-FDR-----NLVN-----EAFMYSHL-----IHNCAEL	1775
CTV	-----RDLFRIVSRRAVACCEYVITL-LKRLAS-----R-AGEYSYSVYVMDTLV-----RHFVANFNL	2009
BcLRaV-1	-----ACALFKDYPEMERSLLRLARHAEFSKRLD-LTMIERFLRCCS-KWRGKYKYNIVLSV-----GSSLYLLKFTA-KATAGGVWDLTWVVARCADQVSRSLVANCGII	1688
CYLV	-----VOGVISCGVGFVRDLLRSFRLL-----LSTL-FIRCS-----RHFVANFNL	1460
CNFV	-----VDFVITCV-----E-----VYVM-YVTC-----RHFVANFNL	1524
MV-1	-----SFGVITALLALLRGLGKFAYDE-----VYFL-IV-----NQLLRPLNL	1556
TV-1	-----ILSSFLAWISKVIRSLYRSIKE-----VKYF-V-----DTQLSHTV	1525
ReV-1	-----VLSSVIRISGAAMRVWRFLVRE-----VKYL-M-----GTIVQDFSL	1522
BYV	-----FLKSSKLVIEACFSAYERIERN-----MKLY-FFPLNSSEEEARRLIRCAGD-----FDYLSDSAF	1569
GLRaV-2	-----SVLAFFSRITWAGARRFIKMKHEC-FGKLFDFLSRLHEFRTRVFGKNRADVGV-----YDFLPTDIV-----ETLSSIEECDQI	1864
AV-1	-----SRLVKQSLSMKGLFQAVQRVKKF-----SSMLNFVK-----YQFVDDVS-ESG-----SSVVSATTS	1666
AcV-1	-----NSLIMKFLDMGRTLVDVS-----VSSISYIKSKL-----	2124
BVA	-----KWKDLCFLFIDMKSSGSMVAKTLNKLKVVVKKLID-----FFTVDN-EPDSSQIEEVGD-----YSSRAVDIK-DSCIRALENL-----PTNEFGSSSN	1758
PeVb	-----VYMF-----P-----	1907
ArPV-1	-----K-----VLKTFREGYLIVRDLFRFSDEN-----LIRSTFYSLEPEVSNHDS-----LFKWSMRHIYKNII-NSSITIFINL-----SNV-FKTYVKFLAD	1282
CoV-1	-----M-----LITLRFKSELQNGIDKSHCKIVLYLLKKNVAVMMFKTKGVCFETLFIIVFNKL-----VNILFRNFVKYFSK	1615
LCV	-----AMVQIVESIFKVFVEIT-----KTSYQS-----LKAIFYKTFE	1230
LTYV	-----SRC-----TVIKSKVEMLFRNKIHK-----IEKF-LQRCGI-----IDQ-YNKIYHMKVS	1133
GLRaV-1	-----RRIVDKGKVVVDY-----EELNMR-KEKCRLL-----	1394
GLRaV-4	-----D-----ISQL-----	1566

F1vA	DERIVDAVRARIGSGYN-----EEEI-----RGYVDCAAV--MFVLRRL-----HSSSIYSKIV-----	1943
F1vB	DEQVMHAKELFGDETT-----SLDV-----RELADAAAVI--VYLVAKR-----RNSWYNRII-----	1692
RLMv	SY-VTNCFTFID----RAPSFLLS-----GRDVLRVISCIFPHISGAFNHS--LYGVLPLGRGG-----SSLLSL-----R	1828
RLRaV	AY-----TLIR-----SNILK-----SADLCRRF-----ERRLG-----ASLRSRSEIDIVLDASVEANVRLPR	1718
SCFaV	AYRISNT-----EHWLR-----AEDAIRCC--C-----GFETR-----SSMEHK-----R	1808
CTV	-----RLYVA-----TDDVVRRCRS--FT--FDCTDKASNFVTGLSWRSLSRGAYSATPGLGGSGRLTSTFSHTGGFT-----R	2075
BcLRaV-1	PKPIRKVFKGVVDV---VRSVYMCRLVLCNPEASGNILLAKV-----SGIDGQS-----LLAQYSKT-----ZSLGLKACYF-----KDSR	1757
CYLV	NLLSEYSTRIRLEVEDHYLKNNTYYLHR-----LSEDVVSQF-----QLERSRSQ-----LRVP-----	1508
CNFV	-----LTTQTVSLVIELOQ-----RSL-----KRSPRPSSTT-----	1550
MV-1	AEFISTLKFKID-----RLRRRL-----NRIPVTFFSAR-----	1586
TV-1	QSMIDSLRCIRE-----FOKRRSL-----NSMPVIGSVE-----	1555
ReV-1	STMISSLYEIRRE-----LLRCRAL-----REVPIIGAVE-----	1552
BYV	-----D-----EDEMRLQAQEQ-----YYSDDESVTYDGKPTVLRSS-----LNVSRRFLET-----	1612
GLRaV-2	EELLGDDLNGVKDDSLT-----DMSYFEFSEDFLASVEEP-----PFAGLRGGS-----KNVT-----	1912
AV-1	VASSENSVDH-----GDQC-----SL-----ALVPHRYLFEFVWVP-----	1697
AcV-1	-----	2124
BVA	RFYILNFIERSRE-----SRRII-----CSERDARLIQEIIVCVRRIQ-----LGLPLHCDVF-----TDLSFVLVD	1816
PeVb	-----VLSKHSML-----VLERIRNY-----LRLPLKFMLE-----	1933
ArPV-1	KEVVQOIFDEVSLKLT--SFCSTSLQM-----IMTGLN-LRTI-----	1318
CoV-1	PELKQILFNNTFELAIT--GVSATSLA-----VLGFINVRII-----	1652
LCV	KMLETDNLMIIDSAAF--TFTNLMA-----VMTGDLNLRVFN-----	1267
LTYV	ILTDVDCFNSVNLNFITH--TGCDALLA-----VLTHGFSIASCA-----	1170
GLRaV-1	-----SEAEIDLL-----IIEKRREE-----HG-----	1404
GLRaV-4	-----VENFNSE-----	1581

F1vA	-----EFAALGSN-----VR-----	1954
F1vB	-----NFFSKCG-----R-----	1700
RLMv	VLCTIFPVGITIAADV-----FF-----TALYSFHH-DAIVYFICGVYLSGGIF	1872
RLRaV	LLAAHWPEYPGFVPECDIISVSDYDDNLTDDCDDDEVLCSSFSWSQLSVITLKGLS-----CLTLALR-----VVFATGVVSCVAYTP	1796
SCFaV	RVSAVVEAMPGIIA-----ALANR-----GVLNLSGNIP	1837
CTV	VIGALGNTLSVVFDEEFF-----RTHLHRLRADVWVLLVEFLKNLP-----VCL-FSIYTFIECRGR-----	2131
BcLRaV-1	WIGTYVDINP-----KERCNGG--YYDYQSDISETEIANVADFEHVMGFDLHDE-----NLACL-TPLNIEVLTRDE-----FAKKM	1829
CYLV	-----KF-----QLVFR-----	1552
CNFV	-----QFG-----RLLRAK-----	1595
MV-1	-----NFG-----AMLWAR-----	1564
TV-1	-----NFG-----SNYFKALYSR-----LLRVLPMVDRNLSDSP	1561
ReV-1	-----F-----CNGP-----KFFVKV-----YNLFRIVANK-----	1649
BYV	-----ILATLEYV-----SY-----	1699
GLRaV-2	-----AFY-----QYHAL--DCVREPWSVALCNLLCRLGSSFTTSYNNR-QIGLIGYNSDRVIQLTTPPP	1930
AV-1	-----VCKKLYF-----VCR-----FOVRQKRKE-----YIEDP	1891
AcV-1	-----CFPPVAY-----SIARYIGHK-----	1958
BVA	-----AIPPVYFLTKRAFA-----	1334
PeVb	-----LSAYLRF-----SK-----	1666
ArPV-1	-----VSSC-----VIEKNLSEK-----	1280
CoV-1	-----LKFMTDV-----	1186
LCV	-----GLIPVVF-----KEP-----	1414
LTYV	-----IF-----	1583

F1vA	-----RNFE-----SVSQMVIKDY-----HKFAELASQ-----KRVRSNAEIEHEK--	1990
F1vB	-----R-----VAALVL-----KCVQIA-----ANYLRKYTR--	1722
RLMv	SA-----FTLC-----HLL-RFLFRDWTPL--SKVANSLE-----DRCRSFLS-----	1908
RLRaV	SATGAT-----IYGVCGPIVGGVLVGCDFHL--NQLSPHLSISLTLTSLYCNLFESV-----FFYPKIA-----LNRVKV-----	1859
SCFaV	S-----DIVALDNAAQSNPNE-----FVWDVIE--GLSINTYQYLSAVAQVYRGAF-----NRRFNEEDERTLRV--	1859
CTV	-----GC-----SFTSELKVFASAGLSFVKTAQVTSISLICESSCTLVGCSLVLTYRVASKADAVLRL--	2187
BcLRaV-1	GLFGGGG-----REVLRVTCVSTYKVV-----VSDLMFFI-----RRRLTSKFSLYYDL--	1897
CYLV	-----LP-----FSEVLM-----RRCVST--LFEL--	1545
CNFV	-----ATEHCH-----TKVSDIRVGVAGMFKVA-----FLDFM-----DRFGSVEYLLFEL--	1571
MV-1	-----CIRYTP-----SLLSTYEDSGFFGIIVRIC-----TKRVL-----RDIDSFEFLLEL--	1637
TV-1	-----VFAFGM-----VIGPTYASAGVTGVLVRC-----LGRVA-----EDCRSSEFLFEL--	1606
ReV-1	GLKGGNEKALLAKFKTCVITACE-----C--VSQICCLRLIRLCWGTACGLVRLF--YITYSSTRVLSRVVAVAVCPV-----LVRNLDGLSDGLTMNGV	1603
BYV	-----CS-----KGPLLVAFALSSALIERF--KGFSRKNKIFTIVREYALSSLRCL--MRALGNDNFVNSFA	1739
GLRaV-2	SVVGSDDIEIEEA-----SAEVEVF-----	1992
AV-1	GSLGRTKKGGG-----	1730
AcV-1	GLSGGCS-----SDELISDCR-----RVM--RFKLLRLKLYVSKMLCWGT--NWCIGLATYISVVRGAVGSAY-----HRRISVFGDELY--FD	2137
BVA	GT-----DTWVPL-----QCSVDCKGAVLKMEEGVGMGLA-----SSYSKSSPITDILTSAI-----	1964
PeVb	-----WFYKTE-----EPPIMPIYTTMGA-----	1988
ArPV-1	-----	1351
CoV-1	-----	1686
LCV	-----	1303
LTYV	-----	1202
GLRaV-1	KCEGKDESEEEES-----EGYL-----	1431
GLRaV-4	-----GAEDKE-----KENTAKSESISSETSEDES-----	1610

FiVa	-----HVPE-----	-----SFKEKIEK-----	CLFM-----	-----SSKYYH-----	-----IYVNLQEIIVSKLRKR-----	ASFLQ	2245		
FiVB	-----YIPE-----	-----NVKLVIED-----	LLFS-----	-----FDRHYY-----	-----LVQKVNFAFFKTOKY-----	FWMK	1976		
RLMV	-----LRFWGS-----	-----RTADRLLS-----	-----VYSA-----	-----FYNPFQ-----	-----FISSVFWAFRNPL-----	AFNTNL	2083		
RLRaV	-----	-----VVGERRAK-----	-----	-----WVP-R-----	-----LVVPIVEWK-RTEPC-----	LRRKL	2043		
SCFaV	-----LLSY-----	-----VQHFGGTL-----	-----GRISDRL-----	-----	-----YFPMR--LKT-----	FTRKL	2047		
CTV	-----LFSVSRLLYD-----	-----SRYFATV-----	-----FSELERLNLYL-DYFLS-----	-----	-----LPKRYLFPNSRARSARVPPVIRTEGV-----	-----	2443		
BcLRaV-1	-----KLPTKDEAFDLISRCFNALGDG-----	-----VWVPDRLTV-----	-----YILR-----	-----TLDFVYG-----	-----RGVSIIREGALRV-----	-----VYRLK	2155		
CYL	-----	-----QKFLT-----	-----PLRS-----	-----	-----ILRKISAFSSYLEKI-----	-----FYTKR	1761		
CNFV	-----	-----RYFSS-----	-----NFPKGGK-----	-----	-----PKD--GIALFFSKTALALENY-----	-----LYTKS	1758		
MV-1	-----	-----RAAY-----	-----NRRGHR-----	-----	-----TYP--VVRKVVEPLFLLENL-----	-----FSKRI	1835		
TV-1	-----	-----RCWS-----	-----KSRLAS-----	-----	-----NSQ--VSDKFFKCVLVYERR-----	-----FTHLL	1809		
ReV-1	-----	-----RVFS-----	-----QLRSAR-----	-----	-----RSC--VFRSLFSYVLKAEEL-----	-----FTRLL	1806		
BYV	-----	-----YDSVLNFIIDVE-----	-----LILLN-----	-----SG-----	-----SVNVLPLVSWRGLSKTAAEA-----	-----IVGSGFASFL	1947		
GLRaV-2	DRFAGY-----	-----SEKLVTA-----	-----EFILKCSPPRALP-L-KTFFE-----	-----GV-----	-----ANSTVSKTVRKLRF-----	-----LVRKFLRK	2235		
AV-1	-----	-----ILD-----	-----ESTVQSL-----	-----RKYIRALS-----	-----SFSSRMHRLNLSNN-----	-----ALNRVFLGSDV-----	-----AVEAVGVEVMIFEL-----	-----FVLKY	1918
AcV-1	-----	-----D-FNLIKKVLGWTMTKDLVSRIPLARRCYPN-----	-----SILMVRKGGYVI-----	-----	-----FSANGKPI-----	-----	-----VSNCSDLHLTPKFDVIFMRL	2401	
BVA	SIYKSARRSWGYPVPS-----	-----IRRFLLA-----	-----MKTNRLVA-----	-----LFWD-----	-----GDSETFP-ATNAGSVLEMLEELDDQSNNS-----	-----	-----VGSNTAEVVEETT--VSSCADV-----	-----IVQSVL	2301
PeVB	-----	-----PNFALYE-----	-----LKEVLK-----	-----LSLPVMVERCSAR-----	-----DADFKLILPMSDVEVD-----	-----	-----VGSNTAEVVEETT--VSSCADV-----	-----IVQSVL	2317
ArPV-1	-----	-----	-----IKYFTTFYSK-----	-----	-----	-----VPLPNCI-----	-----AIST--	-----	1460
CoV-1	-----	-----VMVLVI-----	-----ASKYNAFMER-----	-----	-----	-----AISLANL-----	-----SIAL--	-----	1796
LCV	-----	-----LILLND-----	-----YVKYLR-----	-----	-----	-----VCVKANI-----	-----YLSY--	-----	1408
LIYV	-----	-----IYPAIE-----	-----IKRYNN-----	-----	-----	-----VCFNANI-----	-----KMSY--	-----	1311
GLRaV-1	QA-----	-----	-----RFRVRSNKT-----	-----	-----	-----	-----	-----	1604
GLRaV-4	EG-----	-----	-----MFSIRCNNGSGVLLKPPSWFLMPF-----	-----	-----	-----	-----GFQITHQHSVTCATV-----	-----RVSMTF	1802

FiVa	SK-----	-----	-----	-----	-----P-ILTC-RPVDETHSVRKLAVDVEAL-ENMER-----	2278	
FiVB	IT-----	-----	-----	-----	-----P-GRHQ-EEVPSHTVTAIHLDDIITIL-DDIEM-----	2009	
RLMV	STL-----	-----R-FVHAPTPVDAFQRNGLPFLFDDR-----	-----VWAFSRLCRWLAGDDIPRV-----	-----	-----CNRRCYF-P-VATS-FDLSVPSVEARSV--NFVDSV-ESVLD-----	2165	
RLRaV	-----	-----	-----	-----	-----VLPFCRKYFFLEAAVIRWVW--SCLPIITWKPTRRLLTYPA-LSIK-TYHEDDSEGSAGSSDFISSV-ERTKE-----	2122	
SCFaV	AD-----	-----FMMCSEYSLTAVRIGNFLIRCESQ-----	-----VFEYIKSILRSRGTAKAV-----	-----	-----SVSSQFKA-VSVS-EDDDNFPEAPAVA-KDFLNTV-QDAEK-----	2130	
CTV	-----	-----	-----	-----	-----APVRE-----	-----SLNDLIDL-DSLKV-----	2463
BcLRaV-1	HA-----	-----	-----	-----	-----TGGERSVGSFSA--VPV-TKVGCPVESVTL--QTLDDIVERRG-----	2198	
CYL	VA-----	-----	-----	-----	-----FSKIPDKRPAFLP-VRAY-KSGKEELNGKSSGVASIVESL-EKIAH-----	1806	
CNFV	DA-----	-----	-----	-----	-----NGKTFIGSDRHTPTFEPV-EFTPRIENGL--QVVKPS-ENLEA-----	1799	
MV-1	YD-----	-----	-----	-----	-----EKSSETTSVSY--RRV-EVETRLPSPIVRG--EITTSV-ENLSN-----	1875	
TV-1	YG-----	-----	-----	-----	-----DVETRVNQQLF--RRV-AVSSRVPVINGQ--EIVASY-KNISE-----	1849	
ReV-1	YG-----	-----	-----	-----	-----EPTVQGNRQLF--RRV-AVSAREATCVSRG--EITTSV-ENIAE-----	1846	
BYV	GRM-----	-----	-----CCRVDW-----	-----	-----CSSSSNAGCNFMSPVRTKGGVFPSSSGSTASMYERLEALESDIRE-----	2003	
GLRaV-2	RGG-----	-----	-----LRADGKG-----	-----	-----FHRQ-KAVPIVPSNRIT--TDGVERLSVKMOG-----	2274	
AV-1	-----	-----	-----IRSPVYG-----	-----	-----	-----RVKSKLFDV-VRTY-TPVPSVSDAQR--KYATSEA-EALRN-----	1965
AcV-1	SGGLMGGG--VTSW-SFMLLFR-----	-----LDLLEERNIISCHVNIACKVTACAASSTYRWFMTADWILKR-----	-----	-----	-----IRGW-YLTHGRYHQN--EMEJKP-SKVEE-----	2488	
BVA	-----	-----	-----	-----	-----NAESTVGSASNRQRVSLR-KTVQSHVDACRQF-KDGVAAAM-LKHE-----	2344	
PeVB	SGTLLSDKVFDIRAWEKFLKIFRRE-----	-----	-----DVSFYLDKNRGLRGGSLRGLVFGSALLYL-----	-----	-----VEQF-VSHKVFHPNVIIHIGFVFLNPK-SWLT-----	2403	
ArPV-1	-----	-----	-----	-----	-----	-----GCNINNL-----	1467
CoV-1	-----	-----	-----	-----	-----	-----NEDVRNL-----	1803
LCV	-----	-----	-----	-----	-----	-----GSLVKRT-----	1415
LIYV	-----	-----	-----	-----	-----	-----PHVIDRL-----	1318
GLRaV-1	-----	-----	-----	-----	-----	-----GEIWEHL--LGD-----	1614
GLRaV-4	RS-----	-----	-----	-----	-----	-----TEVITNL-----	1811

FiVa	K-----	-----KMEFLRLAKLVEDQRSETNKSFA-----	-----	-----	-----VNELKDYETPERE--ECEKPNPYTDK-MK--AVSVEE-----	2336
FiVB	L-----	-----KNDFIDRDFVLRSEKKAKEESRF-----	-----	-----	-----VRETLDADDIPI--DVIKDNASSDV-CK--GG--KE-----	2063
RLMV	-----	-----RSSVGLPRREVIDSDSDTT-----	-----	-----	-----SESSTEPLAD--EPVVKASGK-----	2211
RLRaV	ALLFNER-----	-----	-----	-----	-----PKVAPPLVSVPT--IHPVQGAPEE--SVADE-----	2158
SCFaV	LLLVKERLSLRADREKRHHNGKSETAMSE-----	-----	-----	-----	-----AESSSDSEEE--EAVMGASEEK--T--EK-----	2182
CTV	SDL-KGKSTFVDD-----	-----	-----	-----	-----GESDSGSEHS--GSSISFGSNEEVLNA-----	2501
BcLRaV-1	S-----	-----TKDAPLQRKKGSHVTGDKGKGVSETV-----	-----	-----	-----VETSDDSDSLED--TKSVDGTMGN--	2249
CYL	-----	-----TKQAVKTTMKSVRHSETF-----	-----	-----	-----GSEISSGYS--SDEGAADVQ-----	1846
CNFV	MN--ASRLLLRGIIDEAIRRSNQNLTHE-----	-----	-----	-----	-----TPRAED--VD--VPLRSKAEERHD--SESFKGP-----	1854
MV-1	-----	-----LRDELVDLKNAPITNSNGE-----	-----	-----	-----SDPV--FD--TPGEGATGDLRQD--EV-----	1916
TV-1	-----	-----LRSLENLVLDNSIG-KITEE-----	-----	-----	-----YDEV--D--TEEAGASAK-----V-----	1883
ReV-1	-----	-----LRHDDLATFKNFL--PT-----	-----	-----	-----PDR--D--TREDGGSEVE--LP-----	1878
BYV	HVL-----	-----	-----	-----	-----STRCVSGSEEE--ERPKEVTEP-----	2026
GLRaV-2	VEALRTELRLVLEDLDSAVIEK-----	-----	-----	-----	-----LNRRNRNRTSD--EFTRP-----	2312
AV-1	K-----	-----EELIKQIKLNLVSAVSVAWNEV-----	-----	-----	-----LKEVQAKGSSAS--FGADSEA--TDSDEE-----	2016
AcV-1	K-----	-----TVTISEELKTKYSDTVKVAERM-----	-----DELINEMVCRS-----	-----	-----SDDVSGTDL--EISSEDSGNSYKFFNKLKNE-T-----	2558
BVA	V-----	-----EARSMPNSVRQKFTGLLAQVIAEARCSGTMEPNLPYNETSNLIMSNEEWGADGGDEEALLTSRKRKDAKAD-----	-----	-----	-----LSAAEDG-VK--VVDHKN-----	2434
PeVB	QFV-KGCYSNCSNFKSAYNARETRRNSLK-----	-----	-----RYDHVH-----	-----	-----SHDMSDVLHDISVALNSIKADVANNVAKCFPSSIIVEELVT-----	2482
ArPV-1	-----	-----TTSSATKKACKIVQERKFGRRNAPT-----	-----	-----	-----GLKMQNNG--KAEINDQDDEFVT-DNHSEHSEQPVDKQDHP-----	1531
CoV-1	-----	-----SFTSGLRKLVRTLTMQKFKNS-----	-----	-----	-----SNKNG--DLNVQRETKKTES--STALKPE-----	1853
LCV	-----	-----IPSGRYKKLKEIFSSKFKDS-----	-----	-----	-----LFTSKNRGND--HAEGESEGETICR-----	1459
LIYV	-----	-----GGTYNFAKLLKAVREKFSNKSQGVK-----	-----	-----	-----ISEIPEAKDEDVMP-----	1358
GLRaV-1	GDVFMSPGMQRDFKHSVESLDEGRVSTLRL-----	-----	-----NATVD--YCKREATE-----	-----	-----GKRVKGEVTPQ--SRVSVNDGKTSKEAKGL-----	1686
GLRaV-4	-----	-----DGVNRSQLAVRGGSSNSQNHST-----	-----	-----	-----EDKPKGNAST-----	1845

FiVa	-----ANENS-----	-----AVET-----	-----KENLRWADLDDSYEDD-----	-----EN-----	-----ERADLV-----	-----PEIYTNFKDM-----	RRPQ	2383
FiVB	-----	-----AVISP--KVSK-----	-----KETRKWSEIESDDECEILETPKECVDS-----	-----	-----DRADLI-----	-----PAIMKNFKDS-----	RRPS	2119
RLMV	-----	-----ILEPV--GQPA-----	-----EA-----	-----	-----EKSVMGIAESHR-----	-----QETLSNV-----	SS	2248
RLRaV	-----	-----GVGKI--P-----	-----	-----	-----SKIDLMPFAEAKR-----	-----QDEVQSK-----	MQV	2189
SCFaV	-----	-----CEEEI--KVP-----	-----	-----	-----EKTVLHAAEAFAFR-----	-----VLEIGESDSTSTA-----	LRRSS	2222
CTV	-----	-----	-----VNGDSV-----	-----	-----CEKAPLMKHVTA-----	-----LSRLERHPSGRKD-----	IPVSRKT	2539
BcLRaV-1	-----	-----	-----	-----	-----EKDPLIEVAKTI-----	-----LPEVVDVASTSKG-----	NRKL	2283
CYL	-----	-----	-----	-----	-----EKTQL-----	-----PIISEFATPRRE-----	VKHA	1880
CNFV	-----	-----RIEEL--DVPK-----	-----RSSKDNPD--SELP-----	-----	-----EVAQLLYNV-----	-----VPSTNSNPLPRKL-----	ERRRG	1908
MV-1	-----	-----RAEEC--DVPT-----	-----NA-----	-----	-----AVDEI-----	-----PFVAQATEEGKE-----	NERMG	1956
TV-1	-----	-----RVEQC--DEPL-----	-----QA-----	-----	-----ERADLT-----	-----PYSERLENDEKE-----	CSEKS	1920
ReV-1	-----	-----RVAEC--DVPK-----	-----RS-----	-----	-----EET-----	-----PYVADIENAEAD-----	AARSS	1915
BYV	-----	-----GIEHTS-EDVPI-----	-----RSHSQLSGGEGSYSE-----	-----	-----DREEN-----	-----LPHYSKIVSERRGLE-----	TARRN	2084
GLRaV-2	-----	-----AYEQIQ--EVTFTFC-----	-----	-----	-----SKANSAGLALERAVLVEDAVK-----	-----SEKLSKIDEM-----	ARKG	2360
AV-1	-----	-----ESP--PVPV-----	-----QRDCKPT-----	-----	-----ERADTLKVAS--S-----	-----IPNPSLVSEQ-----	RAG	2056
AcV-1	-----	-----DCL-RRENVPKGVSEVRG-----	-----KKKTGRKGNSTPTRYSEEW-----	-----	-----GSDSG--AEGRFK-----	-----VLNITGNEKRFEG-----	KLVDGKR	2624
BVA	-----	-----AKVHF--DEPS-----	-----SSQLRDE--CAEDE-----	-----	-----FSTDS--DMSDST-----	-----LSPITLATEKKGES-----	GVKGVKRA	2491
PeVB	-----	-----KDAVGDENNCK-NKGITLGESSGSYKGGKELISSGECWGDACEASS--GKAGGGDNI-----	-----	-----	-----DSRGGDFIDKILKAATAEPPLVSSIPTVDFEKDVTNEIFESGEKAEPIVTKVA-----	-----	2590	
ArPV-1	-----	-----RPHFERGESS--KPT-----	-----	-----	-----QRTVSEHLQPLAISTLNESEI--SVLDKDN-----	-----	1587	
CoV-1	-----	-----	-----DFKS--GKA-----	-----	-----NSHVKLSEI--EEEI--PSMDNY-----	-----DNA-----	-----RTSSNETTNQLYQKNM-----	1899
LCV	-----	-----VGRTEKA-----	-----	-----	-----SDVEVEL--GYDGEVNV-----	-----KRQKHVNWGSEVS-----	-----SANASDFVDLQFQSM--LKPCVDRTQ-----	1518
LIYV	-----	-----PLEEV--ETPK-----	-----	-----	-----RSVGRPSSKQDDIEDECN--IKEPDT-----	-----ESLNFS-----	-----NIEATSNRYDITLVRGN-----	1413
GLRaV-1	-----	-----LGPVPS-----	-----	-----	-----SGVSS-----	-----SSGES-----	-----VATVRQSASKSTIGTAV--EMGICDPT-----	1728
GLRaV-4	-----	-----DVSLRPQJTL-LTKVKS-----	-----	-----	-----GNGEN-----	-----SLLDVCAKNTGVK-----	-----ITSVSDLLDKESY-----	1892

F1vA	LASS-----SGKPM-----MDSNKGRIKMGSKFLIQLNLC-QDVPMPQPIEYE--KKEFFNTSMRDFYFQYRVALFELFTNYHE-----KYMELVACGFN	2466
F1vB	VASS-----SKETV-----SDDTTRQIGMSKFLQLNTN-QDVPMPQTIIDYI--KKGARFTNSMRDFYFQYRVALFELFTNYHD-----KFLELEACGFN	2202
RLMv	VLPG-----NVPSPRRRSPAKDNVVKICGYLQLNSA-QSVPTGYDRDSSM-SNFSAMTNSIREFYYSQEVTLVLELYSKLFD-----YWFREFVLKHFV	2335
RLRaV	RATQ-----NCIPAKRKTSGSKRGTQISKYLERLNE-EGVPTSYQAEARR-SEFYSMTNSIREFYYSHEVALVLELFMKMSA-----LWEDALIVDE	2276
SCFaV	KSRA-----EVVQS-----KSSSK-----VPMCAVNLQNSM-QMVLNYHEDSSD-DFPRRMTNAMREFYFQYEVTLVLEVYQKMD-----YWADFACGFD	2303
CTV	FVRG-----ESSGVKSMCDYLVTLNSSFGTVPVMPVARD--ITYKCLKNAMREFYYSQKITLYELHGLKSS-----YWDELKVGAFD	2618
BcLRaV-1	KGKE-----VREAQGE-LSPCAYLKLNLG-VTPSPFVAVS-----GKGCTLTNSVREFYFYLQEVAFVYVYCKM-----YYQEANLNF	2359
CYLv	SGRK-----EGL-----CKYLSQNLIC-SRPVPTVQVAPLPGVNSRCTNAVREFYFVLEQVSLFDLHYKFLR-----YWEQLCMDFD	1952
CNFV	I-----CNFLNLQNSY-CVSPYPLVPSDNATHRKCCEAIREFYFVLEQVSLFSLHKLAT-----YFHELNCLFS	1974
MV-1	IDSG-----RIIIPKLRKGNAA-----CCKFLNLQNIS-T--TVPTFSISNS-RSFPMCSNAIREFYAQMEIFSVHKKLLG-----YYEELRAVDNF	2036
TV-1	IATT-----SNY--KRGNSAK-----CCKFLNLQNIS-A--TIPSMRAESL-GFEFPKCLAIREFYQAEMVIFSVHKKLLT-----FFEELSVDVDF	1998
ReV-1	NEVV-----RPV--RKMRSNK-----CCKFLNLQNIS-S--TVPSLSGSL-GTFKRCLAIREFYQAEMVIFSVHKKLLS-----YYEELVDFD	1993
BYV	KRTL-----HGVSEFLNAINTS-NEQRPPIIVDHS--PESRALNSVREFYFYLQELAFELSKLRE-----YYDQLKANVF	2154
GLRaV-2	ATTSEVAVALSDDEAVEEISVAERDDSPKT-VRMSEYLNRLNSS-FEFKPIIVDDN--KDTGGLTNAVREFYFQYMOELALFEIHSKLCCT-----YDQLRIVNFD	2458
AV-1	TSQQ-----FELYLNELNKS-GKLCAPSDYDV--TPYRLLTNSVREFYFYLQELAFELHNRFRIT-----EFDKYEISYFK	2124
AcV-1	NEVV-----RPV--RKMRSNK-----CCKFLNLQNIS-S--TVPSLSGSL-GTFKRCLAIREFYQAEMVIFSVHKKLLS-----YYEELVDFD	1993
BVA	VGRR-----QTKTKVTPGRREEREK-----CKYLNIEGGNITPPSASVMGSDV-----YDKAIGEYVYMNKYAVFTEFDLSN-----KMKLVSADVF	2572
PeVb	KSKG-----LVFSPYCRSLMGN-LVPLAPEMVEDD-----TINARNEYLYLKKQDVYIMYDVTA-----ATTQLSEAF-E	2655
ArPV-1	-----QSFVRLCKN-----PDKIKRCTVF-----KHYPNTITVMQ--NSWEPLTQCFNEYLFEISQTIQLHLKLVSTLANVIRQGFVITP-----1660	
CoV-1	-----VSYAESVNIINK-----TKVCRDL-----LTYPNSSNDFIN--QTSDFLVNALREYIFLEKLNKLNLSLNCVCDIYRSGTVK-----Q	1972
LCV	INCA-----VH-----FPISHAL-----LRYPMTDCDFI--PTGDLNLDDCVSEYHLEAKLHDEMGRVNNVAVRYFEH-----QLETYSKVDKAI	1592
LTYV	-----FELAEVIRNLD--LTCPPVFT-----HTNDPALNAMNEFVFMHMDVMNMLNSMKIASSL-----LWDLKRNPEF--	2184
GLRaV-1	WVLGED-PVL-----GIQSFDN-----VYVKCDL-----KTAGTEAPAEIEMYLAR-RCFDLFIKLRARDL-----VAKTKRVGHK	1795
GLRaV-4	-----KGMKHYV-----SISGNVAVIEAFLY-----NLHELHKEISVISKAA-----LEQPEILVGRK	1940

F1vA	PTLSFSHDCDY-AVMDNRTKCEYTRNSKVNKLTTHIWI--KNNEYVF-----TKDGFVFESEA-----EKYDI-CYGEASFSLSANAFLFKQPN-----AAVTFEN	2555
F1vB	PMLTSFRQSDY-IWMDNIQKKEYTKGKTKLLKSTSHIWI--LTYDFVF-----CRDGLVFSENA-----EKYDY-CYGEASLFLSPNAFLFKQPN-----PLVTFNN	2291
RLMv	RQVCLSHQEDFC-IVDFIRZEMGKYTKGRKSL--KGRFI-----DAYSFGF-----CSDGLPVE-LM-----KGYDY-CLVHTQTFIAANHFNLNSAPS-----RAIKFTN	2422
RLRaV	PLCKATKEDGV-FVINFDQGFAYGANGKRSI-MDGRFI--NDYFVVF-----NSSGLCPTEAL-----KKGKGF-CIVHENQFLAANAFLLNMPSS--RFIEYTN	2366
SCFaV	RKYSKIDQDDKL-FVLDKFLKLIKGSATLNL--KGYV-----SEYQFGF-----CSDGLIPLT-AM-----GRKYDY-CLIHQDKLILSSMLFCSCPS-----RLVYKTN	2390
CTV	RKLTMRDLDDV-YVDFNRKLLVGRNGHPHF--RNTL-----KSYCFMF-----CNDGLVPCPRS-----QKYDY-ALISNQTSVFAANSFRLAGVDG-----KDLFTFN	2704
BcLRaV-1	RGLLTCEMDSKL-VLYDCASRRMQKRRVYKSWEKVYK--EDGFRYCF-----SSDGLVPFTE-----TVRGGK-VVLEHIAFLPQNLFRAYSG-----NFRNFRT	2450
CYLv	RTRECEMEDL-YYVTSNMMNAPKXSRVP--LG-L--AHHEMFC-----TEHGVLNDPK-----YRHNK--LQHEQALFASLNFARGCEY-----HSSVFDNF	2037
CNFV	RAAKCDEADLRLNLSRSCYSSAGKLSK--LREF-----DDHEFCF-----THEGLVNDPS-----SRVDK--LFHESQFLASMSFRSYEN--HKNAMFTN	2061
MV-1	RRACQSDQVLD-SMYPDTSNTHCVGGDNRNG--LKF--SSHOFAF-----TSAGLKPFDKE-----IQKQTHALFHQTKFLAANFLKGFES-----HSTAVFSN	2126
TV-1	RRATQHQVEDL-LVDFPAKGTGINHGRSLQK--IETV-----ADHOFFF-----TRDGLKPNYSK-----IKLDRHALFHQTKFLAANFLKGFES-----HSTLFRFN	2086
ReV-1	RLLAGCHQDVL-LVDPDSKGAANVHSEGRSLV--RGTG-----ADHOFFF-----SRNGLRVPDYCK-----MQLNQAALFHQTKFLAANFLKGFES-----HSTLFRFN	2081
BYV	RQVCLSHQEDFC-IVDFIRZEMGKYTKGRKSL--KGRFI-----DAYSFGF-----CSDGLPVE-LM-----KGYDY-CLVHTQTFIAANHFNLNSAPS-----RAIKFTN	2422
GLRaV-2	RSVAPCEDAQL-VYRKSGSTIVQKGEARLH--IKDF-----HDDHDFL-----DGRSINRKR-----RRGGN-VLYHMDLAFASLNFARGCEY-----HSSVFDNF	2542
AV-1	RKEMLDVDDDT-FVAAGDSVAGFNNSCS--IKEF-----GRHEFCF-----AKTGLIRNSPS-----LKNCR--LYSKHMEFLAERFLAGYPG-----SASFSSFN	2279
AcV-1	NEVV-----RPV--RKMRSNK-----CCKFLNLQNIS-S--TVPSLSGSL-GTFKRCLAIREFYQAEMVIFSVHKKLLS-----YYEELVDFD	1993
BVA	AERYSVIREPVG-YFSTASRKRKIPKPAEKAL--GDYEWGF-----GVNGLTKFNPSRLS-----ELIASKCIIVTEALKHFSSNQLLAGMEK-----DCKEFTN	2661
PeVb	YELSDSAQNSL-IYDQDKKKCGKRA-----DHRHIEYDGLK-----ESDLYCACGKNYCTFKEAMRCSRSRYIHSQMAVYSDKDLMPLTV-----NAVLYTPI	2747
ArPV-1	-----ETKMLNDSYIYKLPNSWESLGRKQVFLK-----KDPVFCSPDVT-----HTENYLDKDSI-----LSTSEFEVGFANRVLKMEAMLETLLMLPTD	1747
CoV-1	KDIAITLVDRAVYMYQPSGLWFLCNSKTKVPL-----SEVFFI-----TADAEIKNSQKDIREG-----CFTDQTSIGYTNRRLFAEG--EHLDKTLYSSD	2059
LCV	WAMRNYFNDSYMYNINSKAYHRLAKDGKDPST-IEAIC-----KYLNDLIDFNTNHLNV-----AVCSDEMGMFSNKRCLALLESILTKSQEIKTIT	1681
LTYV	NVRMRIDRSDMYVTLDGSHVRLGCKDKNPAK-----EDFKATFD-----HFNINMEAKVKEF-----AVSSDEWRGMYNSNKRCLALLESILTKSQEIKTIT	1563
GLRaV-1	FPLAVYENPGL-RVYDANFVWVAPEDGTI-----FDLEYVF--LV-----STGTFVPGRNLE-----AVLSRQDA-VLVCDDLVLVFDHADMNLRGCVR--LAKRALVGEYM	1888
GLRaV-4	REYVSS-----CIPDLRLKVKQCPETLSSVNSLVGSIQKIIIF-----STDKSLETEDE-----VLVLTAPANISFALKRRCIGMFMQMSKLLVDIER	2026

F1vA	ASVKLLVYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVSREEK--KDKAGQVNPATVLSRRVMTVDSYLINK--YAQKCEVLFIDEFCMWHAGAT	2661
F1vB	IDVELLVYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2393
RLMv	ESVKIRVYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2525
RLRaV	AEASRVYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2470
SCFaV	CDIRIRVYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2497
CTV	EEHSLVYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2806
BcLRaV-1	EVHSLVYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2553
CYLv	SNVICMLYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2143
CNFV	TNVDIKLYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2158
MV-1	EDVETIKLFEAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2223
TV-1	TDVETIKLFEAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2183
ReV-1	LDVEIKLFEAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2178
BYV	LDSANVLVYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2338
GLRaV-2	SSVDLMLYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2647
AV-1	PVVV-CMLYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2307
AcV-1	YLNLDLVYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2884
BVA	TLKAAIYVYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2761
PeVb	TKVARIYVYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2855
ArPV-1	SVAELVYVYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	1841
CoV-1	LTSKITLTKPVGSGKTRAIYVNTMVKLIDN--KQSVLALSVTRVGDDEIVEK-SRAHGINR-----TDCVNTVDGFLMN--VKYVSKLLIDEFCMWHAGAT	2152
LCV	RSKDITLYVYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	1775
LTYV	DVNLGKLYVYVYAPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	1658
GLRaV-1	KNVRLSAVNSPPGGGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	1981
GLRaV-4	ATVGCKFINAVPGAGKTHLTLDFIEKSL--KHHTLVLTANKNSSETRKVVVKNA-DK--KLFSPDQVQR--LQSRVMTVDSYLINK--YFRKQVLFIDEFCMWHAGAT	2125

F1vA	LTCLSATKCAAAFFGDSKQIHYIHRNDYGNSTA-----NQHDIDLFLHPDCRLPGTVSYRCPNDVCLWLAK-----EYKHVVSKNKFVEPDVTKMSIVEIDCSEDV	2759
F1vB	LTCLSATKCAAAFFGDSKQIHYIHRNDYGNSTA-----TMVDLDFIKDCKMGLNSYRCPNDVCLWLAK-----EYGHIEKSNKYVDPESKMTSITIDEVGDV	2491
RLMv	CAVLTFTGASLAVLYGDSRQIHYIHRNDYGLSL-----LHDINFLPDSRVYGVNSYRCPNDVCLWSE-----IYPRIQSMNE-KSAGTSSMSVETISCVEDV	2620
RLRaV	AAIINFAGKCAFYGDSRQIHYIHRNDYGLSE-----YHDLINFLPDSRVYGVNSYRCPNDVCLWST-----FYPRHVKSMAR-DSVGSMSVSEITNESDV	2565
SCFaV	TAAFOFSQKAAALYGDSRQIHYIQRNDLGSFL-----LHDINFLPDSRVYGVNSYRCPNDVCLWST-----TYPVHIRSTNE-DSVGSMSVSEITNESDV	2592
CTV	GAVVEFTSCKAAVFFGDSKQIHYIHRNDYGLSE-----VADIDAFIOPEHRYGVNSYRCPNDVCLWSE-----FYPRHVAIANV-GSITGSSVSEITNESDV	2901
BcLRaV-1	LAALFEFTKCAVALYGDSRQIHYIHRNDYGLSE-----FSDLNNIDVGGSGRYGVNSYRCPNDVCLWSE-----QYENKISSAVN-NTVGESSCVATIEIGDCEEDL	2648
CYLv	LAIINASQRRICLFGDSRQIHYIQRNETKSPF-----YGGLSNFIPPSARVYGVNSYRCPNDVCLWSE-----VYKNAKSNIN-ESLGSVATIEIGDCEEDL	2238
CNFV	LMIINSTVNAVLYGDSRQIHYIERCELCCSS-----YSDLENFVRCERTYGVNSYRCPNDVCLWSE-----YSDLENFVRCERTYGVNSYRCPNDVCLWSE-----YSDLENFVRCERTYGVNSYRCPNDVCLWSE	2253
MV-1	LGIINKTMCKVAIYFGDSKQIHYIERDELVSTV-----YHDIDFIEPFCRMVYGVNSYRCPNDVCLWSE-----LYKRRKSNIN-SSITGQSVVNIIESVDV	2278
TV-1	LAIINKTMCKVAIYFGDSKQIHYIERDELVSTV-----YHDIDFIEPFCRMVYGVNSYRCPNDVCLWSE-----LYKRRKSNIN-SSITGQSVVNIIESVDV	2318
ReV-1	LAIINKTMCKVAIYFGDSKQIHYIERDELVSTV-----YHDIDFIEPFCRMVYGVNSYRCPNDVCLWSE-----LYKRRKSNIN-SSITGQSVVNIIESVDV	2273
BYV	VACIEFFTRCHVMYIFGDSRQIHYIERDELVSTV-----YHDIDFIEPFCRMVYGVNSYRCPNDVCLWSE-----LYKRRKSNIN-SSITGQSVVNIIESVDV	2433
GLRaV-2	LACIEFFTRCHVMYIFGDSRQIHYIERDELVSTV-----YHDIDFIEPFCRMVYGVNSYRCPNDVCLWSE-----LYKRRKSNIN-SSITGQSVVNIIESVDV	2742
AV-1	VACIEFFTRCHVMYIFGDSRQIHYIERDELVSTV-----YHDIDFIEPFCRMVYGVNSYRCPNDVCLWSE-----LYKRRKSNIN-SSITGQSVVNIIESVDV	2402
AcV-1	LIFNEILKPMYIYGVDSKQIHYIPRTDLYCVP-----YHNMVMDIEDEGRITRYSYRCPNDVCLWSE-----LYKRRKSNIN-SSITGQSVVNIIESVDV	2977
BVA	LHINKTMCKVAIYFGDSKQIHYIERDELVSTV-----YHDIDFIEPFCRMVYGVNSYRCPNDVCLWSE-----LYKRRKSNIN-SSITGQSVVNIIESVDV	2855
PeVb	LVNFTVRRCERIGYVDSKQIHYIPRTDLYCVP-----YHNMVMDIEDEGRITRYSYRCPNDVCLWSE-----LYKRRKSNIN-SSITGQSVVNIIESVDV	2948
ArPV-1	CYLLANVNTFSDSCDMYDINQTPYICRIPHNVE-----YSK-LTFEMFSEVHDSYRCPNDVCLWSE-----LYKRRKSNIN-SSITGQSVVNIIESVDV	2251
CoV-1	VHLKMYNFTSDSCDMYDINQTPYICRIPHNVE-----YSK-LTFEMFSEVHDSYRCPNDVCLWSE-----LYKRRKSNIN-SSITGQSVVNIIESVDV	1876
LCV	LAVMSLKVTFRCYCDRNPQPIINRAVTCV-----HKH-DTYLTFKIDDSYRCPNDVCLWSE-----LYKRRKSNIN-SSITGQSVVNIIESVDV	1759
LTYV	LTLTKIAYQNGCYVDNQPPIINRAVTCV-----LSR-EFFRKLQNDYDTRYSYRCPNDVCLWSE-----LYKRRKSNIN-SSITGQSVVNIIESVDV	2081
GLRaV-1	QLTVAMGKVIAYGDSKQIHYIPRTDLYCVP-----NEAVEFAE-ELI-----YDTSYRCPNDVCLWSE-----LYKRRKSNIN-SSITGQSVVNIIESVDV	2081
GLRaV-4	ILISAITNPSLSFYDGRQVPPVFNRPVIFRDTVGLMLIKRGDYSE--KLL-----TYRCPADICVYMSITDFLKPGRALVYSGKVTVKD-KRPLK-SVKVTFPSPQD	2226

Fig. S1b. Alignment of RNA-dependent RNA polymerase (RdRp) (ORF1b) sequences of FiVa, FiVb, and related viruses. RdRp domain sequences used for the phylogenetic analysis are marked in yellow

FiVa	SWVRSQATPPRKSLSQENLYSESRNYNFKTGRISSSEKFGKGLAACVVERAFDPEACAKAQRVLTLSVNAAMAKWLQKRSGEKMKLKEFSTP--HEMEDINRFLKLMVKADA	114
FiVb	SLIRSQATPPRIESLQENLSESRNYNFKTGRISSSEKFGKGLANHVVRADFPERYALARRLEILTLSVNSLAKWLQKRSGEKMLVSEMASP--RDLENDINRFLKLMVKADA	114
RLMv	SYRSQATPPRPSLQENLSESRNYNFKICERFSSPKLFGAAMASNLKLLFDAEKLAERQSVISSEANIAKWLKRDASQVKALMTDLDRD--FDIMDDISRFKLMVKRDA	114
RLRaV	GFVRSQATPPRPSLQENLSESRNYNFKSERHCDPKVFGAAMAVLKKCFNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	115
CTV	GVVRSQATPPRKSLSQENLSESRNYNFKICERFVSPSEFGAAMAAVLEKCFMEEMAKIRCDIISL TEANILKWLDRTPCQIKAVHVELKPL--FSVEEQISNFKLMVKRDA	114
SCFaV	SVVRSQATPPRKSLSQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
CYLV	SVVRSQATPPRKSLSQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
CNFV	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
MV-1	SLIRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
TV-1	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
ReV-1	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
BYV	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
AV-1	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
BYSV	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
GLRaV-2	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
BcLRaV-1	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
BVA	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
AcV-1	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
PeVb	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
ArPV-1	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	111
CoV-1	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	111
LCV	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	111
LYV	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	111
GLRaV-1	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
GLRaV-4	SVVRSQATPPRPSLQENLYSESRNYNFKICERFSSPKFGAMAMVLRKCNLEKFPATL RDEVIQVSELATAQAAKRDENQLRNVRDFRFRHLDIGADVSNFLSMVKRDA	114
**.....*	
FiVa	KVKLDASCLSKHPPAQNIMFHDKYINAFSPIDFDEKFNRLMSSLADNIVFFTEMNSDLAEIVRR--IGDED-VYHVAELDISKFDKSDQGVYKAFEEEMYRM--FGFDPELLE	224
FiVb	KVKLDSSCLSKHPPAQNIMFHKYINAFSPIDFDEKFNRLMSSLADNIVFFTEMNSDLAEIVRR--IGDED-VYHVAEMDISKFDKSDQGVYKAFEEEMYL--FGDTEELLE	224
RLMv	KVKLDSSCLSKHPPAQNIMFHRKALNAVSPYCFDEKFNRLYLCPNPIVFFTEMNDLAEIIRRR--IGDDD-IYNGEIVDFSKFDKSDQVFIKFEYERALYEA--FGFDVELLE	224
RLRaV	KVKLDSSCLSKHPPAQNIMFHRKALNAVSPYCFDEKFNRLWLCLNSNIVFFTEMNSDFASVRR--VGDED-IFYKGEVDFSKFDKSDQVFIKFEYERALYEA--FGDFAEMLE	225
CTV	KVKLDSSCLSKHPPAQNIMFHKYINAFSPIDFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--IGDDD-NLFGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	224
SCFaV	KVKLDSSCLSKHPPAQNIMFHRKALNAVSPYCFDEKFNRLWLCLNSNIVFFTEMNDLAEIIRRR--IGDDD-VYNGEIVDFSKFDKSDQVFIKFEYERALYEA--FGDSELLN	224
CYLV	KVKLDSSCLSKHPPAQNIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--IGDQAEQELFVGEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	225
CNFV	KVKLDSSCLSKHPPAQNIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--ISDYDDEVYRIGEIFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	225
MV-1	KVKLDSSCLSKHPPAQNIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	225
TV-1	KVKLDSTCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	225
ReV-1	KVKLDSSCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	225
BYV	KVKLDSSCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	225
AV-1	KVKLDSSCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	224
BYSV	KVKLDSSCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	224
GLRaV-2	KVKLDSSCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	224
BcLRaV-1	KVKLDSSCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	224
BVA	KVKLDSSCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	224
AcV-1	KVKLDSSCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	224
PeVb	KVKLDSSCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	224
ArPV-1	KVKLDSSCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	222
CoV-1	KVKLDSSCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	222
LCV	KVKLDSSCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	222
LYV	KVKLDSSCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	222
GLRaV-1	KVKLDSSCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	224
GLRaV-4	KVKLDSSCLSKHSAQAQIMFHKYINAFSPYCFDEKFNRLMSSLADNIVFFTEMNDLAEIIRRR--VGSDDSLHVGVEVDFSKFDKSDQVFIKFEYERALYEA--FGDTEELLE	226
**.....*	
FiVa	MWMRGEFHGAKTLDGSLRFNVNQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--KPIKNYATVNCNEIGFEMFK	313
FiVb	IWMRGEFEATARDLGRKFSILNQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--EPVKNFATQISNLEIGFEMFK	313
RLMv	MWMEGEYNAHSTMDQSLFRINQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--EKIKHDSHOICLETGFETFK	313
RLRaV	LWMEGEYRAHSTMDQSLFRINQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--TKIANHSOICLETGFETFK	314
CTV	VWMEGEYRAHSTMDQSLFRINQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--EKISFNFSOICLETGFETFK	313
SCFaV	VWMEGEYRAHSTMDQSLFRINQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--NKIANFATEICLETGFETFK	313
CYLV	LWMEGEYRAGAKTLDGQSLFVNDQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--QKLSNFSOICLETGFETFK	314
CNFV	LWMEGEYRAGAKTLDGQSLFVNDQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--TPITNHADAIETGFETFK	314
MV-1	LWMEGEYAAKTLDDGSLFVNDQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--SPIRNHAEAIETGFETFK	314
TV-1	LWMEGEYAAKTLDDGSLFVNDQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--SPIRNHAEAIETGFETFK	314
ReV-1	LWMEGEYAAKTLDDGSLFVNDQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--SPIRNHAEAIETGFETFK	314
BYV	LWMEGEYAAKTLDDGSLFVNDQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--SPIRNHAEAIETGFETFK	313
AV-1	IWMGEFEHSEARTLDGQSLFVNDQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--KPIANVAADICLETGFETFK	313
BYSV	IWMGEFEHSEARTLDGQSLFVNDQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--DEIANYAEDICLETGFETFK	315
GLRaV-2	IWMGEFEHSEARTLDGQSLFVNDQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--SEISNYADICLETGFETFK	313
BcLRaV-1	IWMGEFEHSEARTLDGQSLFVNDQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--NPKINYSOICLETGFETFK	313
BVA	IWMGEFEHSEARTLDGQSLFVNDQRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--REIPDTEISELITDGFETFK	313
AcV-1	LWCAEATEFKARSLDDVDFLQSRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--IMFAAADAVFANCDI GPKFGGGHDTLIFSKGKIPDFSHLIMVDTGEMTKL	339
PeVb	LWCAEATEFKARSLDDVDFLQSRSSGASNTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--EDIVNHAQRNMDIMGEMFK	310
ArPV-1	NFALSEFFCNATASCG--VNDVLCQRDTGSPNTLWNTLTTLALMSVDFADFCCLVLSGSDDSLISY--DPINPKSLDLMNEMGMECKY	310
CoV-1	NFKIYEFYFKARSASG--VKVDLFAQRRTGSPNTLWNTLTTLALMSVDFADFCCLVLSGSDDSLISY--KPIPNQTFNMFKDMGEMFK	310
LCV	NFKIYEFYFKARSASG--VSGELGAQRRTGSPNTLWNTLTTLALMSVDFADFCCLVLSGSDDSLISY--HDLPNVTAENIRDFGEMFK	310
LYV	DFKYTEYDFRACKTAGC--VDLELGTQRRTGSPNTLWNTLTTLALMSVDFADFCCLVLSGSDDSLISY--KHLPNKTEINMGEMFK	311
GLRaV-1	AFFCGEYDFVMTGKNEVLSVGAQRRTGSPNTLWNTLTTLALMSVDFADFCCLVLSGSDDSLISY--NLEQIDRTEIKNESFGDGLK	313
GLRaV-4	TWAASEFYGRATTSSKFSAEIYQARRTGAANTIGNTLVTLSLTCMYDIRKFPFLVLSGSDDSLISY--NPKINQIEVYETKDFDFDKF	315
**.....*	
FiVa	MQNAVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---LTPKELFEVFSFRDLTVEFDQDQIVLERLALLVOKKYEFESGFTLPAALCSHCVRSNFLSFKLFLPHYFGFS	425
FiVb	MPINAVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---LTPKELFEVFSFRDLTVEFDQDQIVLERLALLVHRKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGFGY	425
RLMv	LSPSVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---VTDVLDFAEVSFRDLTRAFDQWMLERLGLVHTKYCTSGFTLPAALCAHCRANFSSFKLFLPFTGVMGL	425
RLRaV	MTPSVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---ITDAGLFEVFSFRDLTRDQNLVVERAVMLVEEKYVNFSGFTLPAALCAHCRSNFSLFKLFLPFTGVMGL	426
CTV	MSPSVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---LTDVLEFELVTSFKDMTQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	425
SCFaV	MSPSVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---VTNEGLFEVFSFRDLTKDYGNDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	425
CYLV	MSPSVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---VEDADLFEVFSFRDLTKDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	426
CNFV	MSPSVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---VDSDELFEVFSFRDLTKDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	426
MV-1	LSPSVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---LTDKDLFEVFSFRDLTKDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	426
TV-1	LSPSVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---LTDKDLFEVFSFRDLTKDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	426
ReV-1	LSPSVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---LTDKDLFEVFSFRDLTKDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	426
BYV	LSPSVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---VDDLEFEVFSFRDLTKDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	426
AV-1	MTPSVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---VDDADLFEVFSFRDLTKDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	425
BYSV	MTPSVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---LSDDELFEVFSFRDLTKDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	427
GLRaV-2	MSPSVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---ASMDLFEVFSFRDLTKDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	425
BcLRaV-1	MTPSVYFPCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---VSDVYKALYESFDKLTTFDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	425
BVA	TRDAPAYFCSKFLVOTGFRVYVDPDKYLLKVLGGFKH---RSYELYERISYFRDTRDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	425
AcV-1	YRDLPAIFCCKFLVOTGFRVYVDPDKYLLKVLGGFKH---VNDVLEYSYKDNCFADFGNEGVRSVLDVNDRYKTEGKTHYSAISVCHLISYNSRFSYDPSIWSFIN	451
PeVb	TKNSYGFCSRFLVOTGFRVYVDPDKYLLKVLGGFKH---VNDVLEYSYKDNCFADFGNEGVRSVLDVNDRYKTEGKTHYSAISVCHLISYNSRFSYDPSIWSFIN	422
ArPV-1	LNPNTPYFCCKFLVOTGFRVYVDPDKYLLKVLGGFKH---LTPKELFEVFSFRDLTVEFDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	425
CoV-1	LDHPTTYFCCKFLVOTGFRVYVDPDKYLLKVLGGFKH---LTPKELFEVFSFRDLTVEFDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	425
LCV	LNRNSVYFCCKFLVOTGFRVYVDPDKYLLKVLGGFKH---LTPKELFEVFSFRDLTVEFDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	425
LYV	TEKSPYFCCKFLVOTGFRVYVDPDKYLLKVLGGFKH---LTPKELFEVFSFRDLTVEFDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	426
GLRaV-1	TCQCAPYFCCKFLVOTGFRVYVDPDKYLLKVLGGFKH---LTPKELFEVFSFRDLTVEFDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	426
GLRaV-4	FDSAAYFCCKFLVOTGFRVYVDPDKYLLKVLGGFKH---LTPKELFEVFSFRDLTVEFDQDQVLEKLLKLVKAEKYNFESGFTLPAALCAHCRSNFSSFKLFLPFTGVMGL	425
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FiVA	LSKFQVYAFSKI-----PNSVV-RLFNGSDSGY-NYIGTVGFGEFDPNQPWESANDVFKGVKFSRRSGGRNSKNFRRLQHLDPQFKSSG-KDVLRADRAK--FYMRSKYE	527
FiVB	LHRSQLRFFSLI-----PNSFV-SVLSTSDRAY-QFLGFVIGEEETPSSEWVACANVTHRVK-TKNPKKYFQKNVRRIRSLPERMRSASFREVMDCKSN--FHEFLRKR	527
RLMV	VTSSRLKFLSLI-----PGLIV-SKAFSSTGESNYFCYLKDSFA-----DDPG-----	467
RLRaV	STYSEIRSLRRL-----VPGLLV-TAYRCAGEKR-YFSYLKSSID-----EDPPPLA--SVVKS-----	477
CTV	VDALKLRLRRL-----TNLIC-ERVVYDNRV-YFSYFDNPFT-KPDANDDNV-----DDLGGAG--ELAT-----	483
SCFaV	VDRNLKFFVKL-----PGIIE-ERVNEERDSR-YFVSLDSEAEATVVS-----QD-----	469
CYLv	FSRVSKSLQKI-----SLGVLQEQKYSTAFGEN-YFLSYTS-----DDA-----	465
CNFV	VKLLPNLKRLL-----FQGLN-CAKVSFH-----FW-----	453
MV-1	VPKINSYFKLLI-----SLGAYH-EKFVTPFGEQ-YFISW-----	459
TV-1	VPKINSYFKLLI-----ALGAYN-ERYVTPFGEQ-YFVAW-----	459
ReV-1	IPRMNSYKLLV-----NLGAYK-EVYQTPFGEQ-YFIAW-----	459
BVv	HYGKLFVLRKF-----ANCFR-EKFDTAFGER-TFLTTKL-----ETVL-----	464
AV-1	FYGRLSKYFKSK-----MNVTK-ERFQTPFGEA-WFLSTELGE-----	461
BYSV	VYGKAKYLKFF-----LGYNI-EPITTTFGDA-WFVYKE-----	460
GLRaV-2	LYTSVKALKFS-----GCSFF-DSYMTFFGQA-VMWVWDE-----	459
BcLRaV-1	VSAISNLMRKIL-----PDFVV-RKYPGVAGVSIIEFLSDLNSSDPHPFRN-----PESV-----	473
BVA	VRGYTHLILLK-----HGKVVYEEKVAKELR-SYVGFVQ-----MYLPDDDCQKL--CDLTTLRAQHGRISYLNSSRG	493
AcV-1	RSVRKVSRLSKFAYYIKLGFVIIDKRDQGDTYA-FDYAFRETYE-----ARNNDVFGKPI-----	508
PeVB	VWHLGAKLMDK-----LGFKEIHENESKDFV-YSKHYGWL-----HHKDEELKCM--SDLSESR-----YAKVTRK	483
APV-1	-----	425
CoV-1	-----	425
LCV	-----	425
LIYV	-----	426
GLRaV-1	KNSKSKATR-----	432
GLRaV-4	-----STGVFK-----	431
FiVA	RKQERQSI FEG-----	538
FiVB	RV-----	529
RLMV	-----	467
RLRaV	-----	477
CTV	-----	483
SCFaV	-----	469
CYLv	-----	465
CNFV	-----	453
MV-1	-----	459
TV-1	-----	459
ReV-1	-----	459
BVv	-----	464
AV-1	-----	461
BYSV	-----	460
GLRaV-2	-----	459
BcLRaV-1	-----F	474
BVA	CKEKKMSKLEKRSA--RKLAVDVDVSNRICA EYS	526
AcV-1	-----	508
PeVB	AEKYLNPRFKKHIVKLLRKMELKGGF--RLTDEG-	515
APV-1	-----	425
CoV-1	-----	425
LCV	-----	425
LIYV	-----	426
GLRaV-1	-----	432
GLRaV-4	-----RGE	434

F1vA	-----LGF-SHKKYDIALVGGSSSLPGVKLSLSSL--YFCNKV-VPFENRAAIVSGCSYKAFDSDNSQLTLIDATSKDLGLASNGKMMLLAPRAAPLPPFNKTSVTCGP	420
F1vB	-----LNF-NNKKFIIITLVGGSSNLPGVKLLKNL--YFCDNI-LDLPDRRAAVSVCALYKAFDSDASLTLVDAASKDGLIASNKGMMLLAPRAAPLPPFNKTSVTCGP	417
FMMAv	-----SKF-RSLKPKVVLVGGSSSLPGLSQTITQM--PFSFGV-VEVPDARGAVSAGCALFVRSFDTADMHLVDCVTVSVSVCSLRGMMAVCPVKGSPLPFVGSKSTILEN	415
RLMv	-----AKF-VNPSKVVVWGGSSSLPGLSGLSLSI--KGISAV-VPLPDHRAAVSVCALYNSCLSDSHSLLMVDCATKTSISIPRYDGSIVIPVAGSPPFDFGERITGMGM	417
RLRaV	-----AGFLKTDVVLVWGGSSSLPGLKELTGLKI--LGVVGV-VSLADHRAAVSVCALYNSCLSDSHSLLMVDCATKTSISISYRGDGSIVIPVAGSPPFDFGERITGMGM	419
SCFaV	-----ARFSAEHGAKVWVGGSSSLPGLCDELNAV--HGISGL-VLRLDHRAAVSGCALYAKLTSANVLMVDCATSNICLPGTCAOICVWIPVAGSPPFDFGERITGMGM	416
CTV	-----SSMPSESQSLKLVWGGSSSLPGLLDALATV--PFVSGI-VPVEDARTAVATGICALYSECLDGRSKALLIDCITHTLVSVTTFADSVWVAAGASPPFDFGERITGMGM	418
BcLRaV-1	-----AGFTGERNTTLVWGGSSSLPGLHEELKKF--LVVRKI-VLPDRRAAVSVCALYNSCLSDSHSLLMVDCATKTSISIPRYDGSIVIPVAGSPPFDFGERITGMGM	417
CYLv	KIPRSGEKKEKTSDDGCVLITVGGSSSLPGLKGLLSAI--PYVSRV-TELDPARRSVAAGCAYMSYCLACKDSSMLLDCAASHLSIPSYQCESIVLVAGAPPPFDFGERITGMGM	437
CNFv	RV-----GEMSSSEKCVLAVGGSSSLPVLNLSITSI--PYVKRV-TELHDARAASVGCALYNSCLSENSPMLLDCAAHNLSIPDYKLESIALVPAGAPPPFDFGERITGMGM	432
MV-1	-----STMNHDRKCSVTVGGSSSLPGLKNVIEAI--PFVNRV-VEVPDARSVAAGCAYMSYCLACKDSSMLLDCAATNTLTPSYCTETIWWVKGAPPPFDFGERITGMGM	429
TV-1	-----GVRKEHHRKCGVAVGGSSSLPGLLVLSAI--PFVDDV-INLPDARAASVGCALYNSCLCKESMMLLDCAATHLTPSTYCTQSIWVVKGAPPPFDFGERITGMGM	430
ReV-1	-----AASIDHHRKCGVAVGGSSSLPGLMAVLSAV--PFVNAV-IMLPDARAASVGCALYNSCLCKESMMLLDCAAHNLSIPSYLQCSIWVVKGAPPPFDFGERITGMGM	430
BYV	-----MRLFENAKKLVAVGGSSSLPGLLSLSSI--PFVDEC-VLPPDARAASVGCALYNSCLSENSPMLLDCAAHNLSIPSYLQCSIWVVKGAPPPFDFGERITGMGM	424
BYSV	-----AQAASLVLVWGGSSSLPGLKSLQSV--DFVSEC-IDLPDARAASVGCALYNSCLSENSPMLLDCAAHNLSIPSYLQCSIWVVKGAPPPFDFGERITGMGM	425
GLRaV-2	-----AQTCDLVLVGGSSSLPGLADVLLKH--RSVDRV-LRVSPPRAAVSVAAGCAYMSYCLACKDSSMLLDCAATHLTPSTYCTQSIWVVKGAPPPFDFGERITGMGM	424
AV-1	-----EGRPMMTKASVILVGGSSSLPGLDKVLQGT--DFVSGI-VKLNKRAAVSVAAGCAYMSYCLACKDSSMLLDCAAVKHISINAWNGEAITLVAAGSPPFDFGERITGMGM	426
AcV-1	-----SGL--QGDITLPIVGGSSSLPGLISAKMYL--NKIGTE-LVYPRLRITAVSSECCVLSVATV-GIPGYLVDCITTSISGVTFFCVTPPLIPRSGAPPPFDFGERITGMGM	407
BVA	-----TGW--KAPVEVYLVGGSSSLPGLVVDKTROR--PYVSEV-FDLPEKRSVAVSVCALYNSCLSENSPMLLDCAAHNLSIPSYLQCSIWVVKGAPPPFDFGERITGMGM	418
PeVb	-----SDM--KTDICLVPVGGSSSLPGLVAVQAQSEIRKMGRT--LVYPRLRITAVSSECCVLSVATV-GIPGYLVDCITTSISGVTFFCVTPPLIPRSGAPPPFDFGERITGMGM	409
APV-1	-----NN--LTTFTSINMVGSSSLNLIYNAVNRFGSKGAKV--YRDNRLRLVALGCACLFS--LESDPEFTYIDVNSQPLYDGLYHYPELVKRPMPVPTHTVSHDNL	406
CoV-1	-----NE--ITNAVTCMVGSSSLNLIYNAVNRFGSKGAKV--YRDNRLRLVALGCACLFS--LESDPEFTYIDVNSQPLYDGLYHYPELVKRPMPVPTHTVSHDNL	408
LCV	-----NK--VSSGALFLVGGSSSLPKIQEDVKAFAIRYKIEC--IVDKDRSAVSGGCSMSHA--QEDTGNMTYIDVNSQPLYDGLYHYPELVKRPMPVPTHTVSHDNL	410
LTYV	-----NK--LTSGVYMWGGSSSLQPVQWVRYSYATKGLTL--VAQQDMRSVAVSVCALYNSCLSENSPMLLDCAAHNLSIPSYLQCSIWVVKGAPPPFDFGERITGMGM	411
GLRaV-1	-----LK--RSPITVCVLTGGSSSLPVLQVKLKTLL--PYVSRVTEYDSTKFRLLSVAAGCAYMSYCLACKDSSMLLDCAATHLTPSTYCTQSIWVVKGAPPPFDFGERITGMGM	415
GLRaV-4	-----NN--VNSCAAVLVGGSSSLPGLVGRNVSASL--RGVSRVIFDKDYSVAAGCAYMSYCLACKDSSMLLDCAATHLTPSTYCTQSIWVVKGAPPPFDFGERITGMGM	409

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F1vA	KVDSSELLIYLYEGRSTRVLYNELLASTKVLCSQLNGTSTQTA-IDMWHYETQISTTGRV--TCKVSGENGVIITIH--VQSVDYDFEGRELL--KLSITNEQTQDRDLIDAISVI	528
F1vB	KKPSSLIHVICIYEGRYSRVLYNELLASTVVICSELIHTIDKA-VDIVLYSVETMISTTGRV--VCKITGSSQSVTLQ--VQSVDFDSSVILP--DMKVDDKEERLRGFVNNLFL	525
FMMAv	LTRSAPIRIFKFEFEGESTRVRVNDPLFAFEFYLKQMDLDAWIS--SLLKVTHTTEVSSVGEV--SLRLSAANS--SLDMK--PSKLVDFTPTSPK--IPHIVNDRKELDSIKNFIAL	522
RLMv	CSKTAHYNRILFEGDHMLCAVNDLIIYSAEYVSSLVQVQATP--ISVNLVLTVIDSVGKI--SFSIKGPSVGSVTPVQ--GRAHYDFTLPL--KSVVPLRSSTDKDLASLVALL	525
RLRaV	ATTSTSTYNARLFEGFMKCAVNEIYKSTTELRSLVGVAQQP--TSAKLKLTLKIDSVGKI--SFSILGPSGVPPYVQ--GKPHYDLNLSKGP--QRNLVRLNAKLRRETRILLCAV	527
SCFaV	ASINSYDARLFEGNYTKAPRNELIYSSRVLKDLGLNLRQT--TTVYKLTHTKIDSVGKI--SFSIKGPSVGSVTPVQ--GLPHYDFTNLSKGP--QRNLVRLNAKLRRETRILLCAV	525
CTV	CVSTSNYQARMEFGDEYKVFNRERIIYAASTLFTLVGNVSWP--NDVMTLVTKVDSMGKV--EFLYKGPSGELVNVQ--GTSYDHYDAGMPPH--TRKLVRLSDYNNVSAALVLL	526
BcLRaV-1	TGPTSTFTIAMFEGDSEHCRCRTRFVSDVNLKDLGVTHNA--R-FRDNELRLVTEVDSVGI--KCYLKGNGILVDTE--SKPHYDFKGNCP--SRRLVSSDAEDMKVRLMT	524
CYLv	ASATSSYNAITLFGDYSKCPMNERIYSSATQLKDLGITAVRP--VTRSTITLVDVSVGTI--TFVKVGEKGAEIVG--KDRMDFDSGCHSP--TRSVNMLFKNAERVRLNLVL	545
CNFv	AAATSTYKASLFEGRDKCMQNELIYSSITLSDITGVQVA--T-----	475
MV-1	ATRSKFFVAALFEGYQKCALNELIYSHVPLSELVGTSDLP--RSLPMTLEQVSISSVGTI--KFIDIITDGRRTYVG--KDRPYDFSRRNAP--SRNVWRMSDQLRRTSIISLV	537
TV-1	VRPNRFRVAALFEGDHKCKGMNLFSSVYPLHEIGVTDSTP--NRVSILEVSISSVGTI--KFGLIKNOGELYTVG--KDRPYDFSRRNAP--SRNVWRMSDQLRRTSIISLV	538
ReV-1	YNARAKFVAALFEGDHKCKGMNLFSSVYPLHEIGVTDSTP--NRVSILEVSISSVGTI--KFGLIKNOGELYTVG--KDRPYDFSRRNAP--SRNVWRMSDQLRRTSIISLV	538
BYV	SNASAVSVAALFEGDVKRCLNKRIFFGDVLGNVGTGSAT--RTVPLTLEVDSVGTI--SFSILGPSVGSVTPVQ--GRAHYDFTLPL--KSVVPLRSSTDKDLASLVALL	532
BYSV	CVGSGSYVPLFEGDRTKCFYKVKVFGVTPVGLKDLVGTDP--RTVPLTLEVDSVGTI--SFSILGPSVGSVTPVQ--GRAHYDFTLPL--KSVVPLRSSTDKDLASLVALL	533
GLRaV-2	ANKNSQREIAVVEGYYKCPKRNLCIGANVKKFDIGVASTSY--EPYVYMDTFISSVGTI--TCSLVGPTGVELSTQ--GAPSYDFSGSAP--LRVVADNHDFNFRRLTALL	532
AV-1	ASANASQREIAVVEGYYKCPKRNLCIGANVKKFDIGVASTSY--EPYVYMDTFISSVGTI--TCSLVGPTGVELSTQ--GAPSYDFSGSAP--LRVVADNHDFNFRRLTALL	534
AcV-1	---NYNRYLIAMFEGDSEHCRCRTRFVSDVNLKDLGVTHNA--R-FRDNELRLVTEVDSVGI--KCYLKGNGILVDTE--SKPHYDFKGNCP--SRRLVSSDAEDMKVRLMT	512
BVA	---TGVRFTITLFEVGGSSSLNLIYNAVNRFGSKGAKV--YRDNRLRLVALGCACLFS--LESDPEFTYIDVNSQPLYDGLYHYPELVKRPMPVPTHTVSHDNL	503
PeVb	---KTSYFSSVGGGNDRLVFLNKIAAFVTVVDFPLMADAVGVESSWHLKLNKLMGMFSGYTRTAGYPOERELTV--APRVLTLQTIKQN--LRSDAYFTSELTIAVKDYL	518
APV-1	---IYKGTICVLEGGDAPWLEADPLVNTSISTDIVSKAGE--GFWYHYIYADVTGI--NWIENSKDHKVQVQL--QNQLQESFEFKL--ELERVOYGVN--TEVMTDII	505
CoV-1	---KFLTAVIDYEGDSQWFLDCQVLLTKDQVYSDAVSSLSG--GFWYHYIYADVTGI--NWIENSKDHKVQVQL--QNQLQESFEFKL--ELERVOYGVN--TEVMTDII	507
LCV	---HYSITLVWVGGSSSLPGLVNDMLISARMQSSLVYCNVGD--TIEYLKYNDVIGI--ELSVNKTITGKTEVL--PMTFTLTSKTKL--DLSLTLQSN--DETATLIAL	509
LTYV	---PLKTIYVWVGGSSSLPGLVNDMLISARMQSSLVYCNVGD--TIEYLKYNDVIGI--ELSVNKTITGKTEVL--PMTFTLTSKTKL--DLSLTLQSN--DETATLIAL	510
GLRaV-1	---STMEYGIIEGESNRVWLNELTAFKQ--TIDYRPSNERK--SDKVKYIEISVDGKL--KLSVDGRQLKNTLRLPAPVSAHAHYRVSSM--KYLQLQEN--DKRIKPEVDD	504
GLRaV-4	---YNTGVVLEHEGSSFINENARTYSAPLKTITQFP--GGKTYVNFVISEDGRL--EVLKNGELANTVVPESPAANEYSERFLSSD--DKRIKPEVDD	499

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F1vA	SYRKICKVDVSR---DRL-VIKELSE-----LQGSSEL---VGGYK---LNDEEKLKISMSVLRSTFPVGLRRED-----VSFVPPFEV-----	594
F1vB	SFGNYLNNISIAI---NSL-RLEDLSN-----LDLTSL---AKIYN---IDVEKLHPAEMVLRSDFPVGLWRNN-----VSFLPFRR-----	591
FMMAv	ASINPQARNNKA-----LSDTSVLSSTPSSHVFIDTAA-----AGPSEFDAELVLRQTVPRNVRSS-----VRRVPPFG-----	588
RLMv	TQEIEARNDLHQ-----YLDKLNLSAIVTIPS--LSLEDHG--KAGTFPT--LTNGRVAKSRACMGKVPKTLRGTN-----VLVPLQDQ-----	599
RLRaV	TINGVCRQSVPL-----FKTQLDEVLVKSPSADDDLLAL--LQAVPY--ITSECLNVADSRMGELVSGRLRGTD-----VESTPF-----	596
SCFaV	TLDPPEARASVYFH--KED-YLCEINDA-----KPLETY--RSKYDV--ASSYRISERSRMGKAVQKILRGAA-----VERLPL-----	592
CTV	TLTREKREKFLRLLFDL--LLADLRKT-----ASLGEY--SKYP--ITRNDIDVSSRMGIVVSKVLRGSD-----LERIPL-----	594
BcLRaV-1	SRDSDDRNRCKRY--AQD-IVTIVATG-----VSFVEA--SQHSK--LIRNDISEAVDLLGRPFQVLRGGR-----VKRISIGGSS-----KL--	598
CYLv	TRTPEARSRLSLS--EVD-KLYNENRD-----YQLQIL--KRDYPN--FNVDVTDVCRSLMGVVFQKILRGRS-----VERLPL-----	612
CNFv	-----	475
MV-1	SRSERVRSIRED--VRQ-KIYSEPE-----LAPNDV---VVQCG---LNDEEKSDCAKYLDSSVKGIVRGAS-----ILKLDLD-----	604
TV-1	TRHERIRENLKQ--QLD-EIQERGSA-----LTSQEV--ARKLG--LTTDEVNDCDEYVNNIDKVVGRSS-----ILRLED-----	605
ReV-1	TRYIHTRERISED--EMV-RFQSQSST-----LTRVDT--IKRFA--VKPEEADECEYLVNGKIEKEVRGSS-----VLKLED-----	605
BYV	TYQPFQRKLTG--DKALFLKRLT-----ADYRRE--ARKFSS--YDDAVLNSELLEGGRTIPKILRGRS-----VEKLDV-----	598
BYSV	TKTREARQKFSY--EKQ-HLDSLSGN-----LDTEKE--SKFNG--YNEQTADVCRIILGKSVQKTLRGAR-----VEELSYRNYEVQV---LKT--	611
GLRaV-2	HRKADRRLFTK--EAI-RYTESIDI-----VDVLEK--YKSYAA--SALPPDEDVPELILGKSVQKTLRGRS-----LEEIPL-----	599
AV-1	TRTLASRLKTA--ETP-RLSL-----PNLSV--KNSFG--SNEQYEDVCGVLMGKVPKILRGRS-----LQKILRG-----	599
AcV-1	SQSIKAVPKIAVDNITA--YLRYLRETQG--SDPPEVE--FKHYG--SNEQITKSVGLIERRPVPVFREEG-----VSYVPR-----	584
BVA	TYTMDQRDSIAVKGGRD--YANVISAA--PVFMGTG--KLSNFTPNQLSGEYISMLLSARGEETSKLSRSGKICACDRDATIDEEMKSLRPFPLTGYCDSVSVLKL	606
PeVb	SSLVKNDVEEV---NVDS--YKDFLDRGHIG-----LLGFNAKSLNLDYAGADALLATRPVPDFLRATG-----YREIRR-----	585
APV-1	KHHPGQDFASIDLNFPNLLKLYVNDHGG-----ISRLDE-----ILRDIL-----	546
CoV-1	KYHKLKDKNIEADSNLFFKIKDYIEINGG-----ISKYIE-----TLRKNG-----VQI-----	551
LCV	SHFKPDLKHLTYVKTPTIFETKLNISS-----TKELYS-----TLVGLNK-----NFKNK-----	556
LTYV	GYHDKNFERFYGLFNVPTILKEIDKLG--FKTLYR-----RLKSMNA-----NF-----	554
GLRaV-1	-----YVDMFSELHGDK--ISIDVYDATGAYFD-----KNILVNFRLSK-----	543
GLRaV-4	-----TKSFYS--RILGDSNLKN-----RDLRGRK-----EQYCKHGIV--CD-----	533

Fig. S8. Alignment of coat protein (CP) (ORF8) sequences of FiVa, FiVb, and related viruses

FiVa	---MAT-----TPSKDAQDLOQIATTP-----PPSAPPQSTPPPQNSLIAGAGSTIVNTELLESHL FVSDIRKLDE--KKEEMANNHFRSCLTNVGFIPDKAEAFKAALPAI	98
FiVb	---MADKVDNQSGYVPLASE--KSSLTLP LPKKDNSSQSSYAPPKQDQDIPGAAAISSQPVGVSSV FVSDVRK LNS--VNLARAN EYFKRSL EGGKFGSIQDKSEAF E VALPAI	108
FMmAV	---MAGSTDAQSTSNSSSTS-----LVSA-----PSNALSSKLVPIENTL--QSLNSVLDRLDISISIQTRPKDYKTE--EEMRHYLD EIKNHMITV--YKID EKD--YMIHLTMI	93
RLMv	---MAE-----FTIADLKEINVADNTLSE--EVEAKTKP L LAKIETANPGFDDK G--AKL LVGMT	55
RLRaV	---MAL-----VDFDTLGTIVVADSTAMSF--EGSKVAEEVLFELKTKNNLFDV D K--LKTHWAMV	56
SCFaV	---MPE-----VRYSDITGLSVGNSTATNT--ADAALVAKDILAKVKETNP TLTDH--LNLIWGVV	55
CTV	---MDETKK LKNKNK ETK-----EGDDVVAES-----SFSSVNLHIDP TLITMNDVRQLST--QQNAALNRD LFLTLKGGKHPNLPDKD--KDFRIAMM	83
BcLRaV-1	---MELSRQFVYIIRTADYDFIEITRRSLVWTLTFERSKMSTGKP-----S L T L S D I G N V S V K L D K E L N E--K E L A I V S A G L V K I L T E E--Y K F K A D D--V L L H M Y M I	94
CYLV	---MPE-----NDSNDSSNKS-----A L T Q T P S K L S S V S I S D K R L L T G--A V K D A A K I K F F T G I T A K Y P S I N I A D--T N T H L G M L	68
MV-1	---MVD-----TAGKLAVIDAFNVEDERIISVSDLAETRQKFEK FVTDK--LQGD L K D--L D L H L G L I	57
TV-1	MLTTMPADEK-----S--NSEVPI L D S F K V D D E R I I S S I E D I V E I T K G I S K F I V D T--L K G S A D Q--L D L H L G L M	64
ReV-1	---MPAEDK-----NVESEVLVDSYKVDDE R I V S S T E D I V A I T K G F S D F I T N V--L K G S G E Q--I D L H L G M I	61
BYV	---MGS-----A E P I S A I A T F E N V S L A D Q T C L H G--E D C D K L R K N F E E C L K L K--G V P E D N--L G I A L G L C	57
BYSV	---MAGND-----E G S D D S S A S Q-----T M T A K D M I F A P F E N F A R A S A T C L N G--E N K K L F E E F S V R V K T Q--D V T E S G--I P T T L G M T	72
GLRaV-2	---MEL-----M S D D N L G N L V I T D A S S L N G--V D K K L S A E I I K M L V Q K--G A P N D G--T E V V F G L L	53
AV-1	---MGDAAKL LAAKNA-----AGGT D G T T D D-----A G Q T L G R L L G L T F G S P V L K T G--N D K V L K L L T G E F M V S K--G A K P G E--V S D A I G L L	76
	* : : :	
FiVa	LYFFRIHTTSGEAKH--EQTSVNFVL--GNVVRTISESDLIEAAKTC PQL--RMYSNSIRAWCRSNEKTYIDYSRQNP D--LPSSARATRIGLPAHYSWLEADFLTG--EHL--TDEERA	206
FiVb	LYFCRIHTTSGEAKH--EQTSVNFVL--GNQNVNIVERDLVETARNCPQL--RTYSNPLRAWCRSNEKRYIEYSRQNP D--LPCSSRATKIZGLPSHFSWLEADFLTG--EYL--TDEERA	216
FMmAV	IYRLAVVSTSDKRYS--SPHDHIKYV--GGTSYKLYDNAIIPYKLNLMHD--PDVRNPLRKF CSTAESL L V I A A I R P D--L F E T H R A T R S G T P M H K G W L S A D F V G T S S P L Y S E L D R S	204
RLMv	LYRLALRTTSPNATF--NAHDVTTYKV--DGKSVKFDDEMVFYIANHEAIPP G I K N P L R A W G R A L D Q Y K L F I R P L K T T L D F N Q R C N K I G L P V G Y E L C A D F L T G--A G L--D N Q E A A	166
RLRaV	LYRMALLTTPSLAKL--SNEITSYKI--GDKEFSFSDQVFNFKLNHPKS--SKYPNPLRSWGLGSE TVYLD F M R R K D T L H F T S R A T R I A L P E G Y E F L C A D F L T A--N N L K D N K E R E	166
SCFaV	LLRLAVRTTSEKSLG--FEETTFKI--GDVEYKIKDED F V N V D K H V K T--R F E K N P L R H W A R G S N A A Y L D I A R K T P N E I--M S A R A L K C G L P K D V G Y L C A D F L V G--S G L--S D F E R T	162
CTV	LYRLAVKSSSLQSDS--DATGITYTR--EGVEVDLSDKLWTDVFNKSGI--GNRTNALRVWGRNDALYAFACRQNRN--LSYGGRLDAGIPAGHYLCA D F L T G--A G L--T D L E C A	191
BcLRaV-1	MPLLN RVSTSEKVVASQAGSGISYTL--GGAEYALKEDI LSK IADLVP--RTGKNLRLWARSRESMYLDVAF AQPD--L F K C E R S L K A N A P N G F A W A S A D F L P G V D H R L T D E M R A	204
CYLV	LHGVAIKTTSKQASE--PEGEFVNYTL--GETEYSFTEKDYLNIFDSIPRI--TGNNPRVFCRSFATEYLDFF L K N S T L P N N P R A L S O G L P P G V H Y L A A D F L A C D C K L--T L H E A A	178
MV-1	LVAFAIKTTSRQAVK--GDAEFVNYTL--SGHVSSTATEKDIT E F L N S L P Q L--K D R K N K A R V F C R S F A K E Y I K T C R S H A N S L P K Q T R A I K L G I P D R V H Y L Q A D F V T D C S E L--T D E E Q A	168
TV-1	LYACAIHTTSSKAFR--PEGELTSYTL--SGRKHVNTRDFLEFLNLSL P Q L--S G K T N K I R V F C R S F S N Q Y L A V C R E F G E K L P Q V R G T K L G I P T Q V S Y L Q A D F I S D C A G L--S E V E Q A	175
ReV-1	LFACAVRTTSSKAFS--TEGILAEYTL--SGRKYIVHARDL L N F I N S L P Q L--N A R V N K I R V F C R S F A N A Y L S V C R A Y S Q L P K L V R C T K L G I P A Q Y S Y L Q A D F I S D C S E L--T E H E Q A	172
BYV	LYSCATIGTSNKNVQPTSTFIKASFGGGKLYLTHGELNSFLGSKQLL--EGKPNKLRFCRTFQKDYISLRKEYRGLPPIARANKHGLPAEDHYLAADFI STSTEL--T D L Q Q S	170
BYSV	LYALATLSTSSKIDIEDKTP L V S A K I--DAVNVTI TYED I K N F V N S L T L L--K N Y K N K L R V F A R T F E E E Y L R F V R Q Y K H I L P N I A R A N K H G I P A D Y S Y L A A D F V Q T S N L L--K E H E Q A	184
GLRaV-2	LYALAAARTTSPKVQRADSDVIFSNRF--GESNVVTEGDLKKVL D G C A P L--T R F T N K L R T F G R T F T E A Y V D F C I A Y K H K L P Q L N A A A E L G I P A E D S Y L A A D F L T G C P K L--S E L Q Q S	165
AV-1	LHAYNIRSTSPKVERD V D I L F S A V L S A G S A I V L E G E V N A W L N N Q S E L--K T H V N K A R V L C R T L G D E Y I A F L R E N H S V L P P V P R A N K H G I S A A H S Y M A S D F Y T S N K A L--S N E E Q A	189
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FiVa	ALMIATKVALSRAAVTPE--AKIISLTQLGRV-----	236
FiVb	ALMVATKVALSKSAVAPE--ARIISLTQLGKTIG-----	248
FMmAV	MLLRSREVNLSRSTRDRS--GVLVSLDL DGN-----	233
RLMv	ILNLGRAEALKKEVGDTG--HSITSIKQLGRFST-----	198
RLRaV	IWR L A R D M A L T P K E G S D P V--Q S I T S L T Q L G L K T Q G G L Y R	204
SCFaV	CYLAQNHMLAEKAGIPAT--GTLTTIANLGY YKA-----	195
CTV	VYIQAQEKQLLKRK G--ADD--VVVTVNRQLGKFN T-----R	223
BcLRaV-1	AIVSCRKTL L K R S K E V N E I G H Q L I T L E R L G V A S-----	237
CYLV	AAVKAKDHALASKQ--VAD--QFVANVY E I G K H-----	207
MV-1	VLLHGRNHAVAPINSAAT--PIVTNLYELGGGKR-----N	201
TV-1	VLIKGDIALKSAAVGT--TATTNLYELGTHSR----T	208
ReV-1	VLVGRDRALNPVTGAGA--SSVTNLYELGSRSQ----Q	205
BYV	RLL L A R E N A T H T E F--S S E--S P V T S L K Q L G R G L T G T--R	204
BYSV	VLL E G R N A A T A S S G--T T R--E S A V N L K Y L G G S S K-----	215
GLRaV-2	RKM F A S M Y A L K T E G G V W N--T P V S N L R Q L G R R E V-----M	198
AV-1	VHLHGSNHALKTEG--KEV--TEITSLFQLGRH-----	218
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